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## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

## STAFF USE ONLY

## Type of Search

## Vendors and cost where applicable

Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>if Contact: Sheppard</u>	AA Sequence (#) _____	Dialog _____
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Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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RESULT 9
Q9UL83 PRELIMINARY; PRT; 110 AA.
AC Q9UL83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Makiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206023; AAF69321.1;
DR InterPro; IPR003596;
DR Pfam; PF00047; 1g, 1.
DR SMART; SM00406; 1g, 1.
FT NON_TER 1
FT 110 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 64.7%; Score 413; DB 11; Length 110;
Best Local Similarity 72.1%; Pred. No. 1,4e-36;
Matches 80; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 10 ELVPGASVTKSCASGYTFNYFYWKORPGGLEWIGINRNDPTDFNEKESRAT 69
Db 2 ELVPGASVTKSCASGYTFNSNMNWKLRPGGLEWIGITPGDDAYNGFKKAT 61
QY 70 LTVDDSSATVMOJLSLTSEDSATYCTSPYGNNGFTYWGQGLTVVSA 120
Db 62 LTVDDSSATVMOJLSLTSEDSATYCTSPYGNNGFTYWGQGLTVVSA 110

RESULT 10
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; Pubmed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.;
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
EMBL; AF035022; AAD56258.1;
DR InterPro; IPR003506;
DR Pfam; PF00047; 1g, 1.
DR SMART; SM00406; 1g, 1.
FT NON_TER 1
FT 124 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 64.6%; Score 412; DB 4; Length 124;
Best Local Similarity 62.1%; Pred. No. 2.1e-36;
Matches 77; Conservative 19; Mismatches 24; Indels 4; Gaps 1;

QY 1 EVOLQSGAEIVKPGASVTKSCASGYTFNYFYWKORPGGLEWIGINRNDPTDF 60
Db 1 EVOLVESGAEIVKPGASVTKSCASGYTFSSYMHVYRQAPGGGLEWIGINRSGSTV 60
QY 61 NEKFSRATITLVKSSSTAVMOJLSLTSEDSATYCTSPYGNNGFTYWGQGLTV 116
Db 61 AOKFGQVMTVTRDTSTVYMWELSLSESDTAVAYCARGLYVVPAAFSRFDYWGQGLTV 120
QY 117 TVSS 120
Db 121 TVSS 124

RESULT 11
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; Pubmed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.;
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
EMBL; AF035019; AAD56255.1;
DR InterPro; IPR003506;
DR Pfam; PF00047; 1g, 1.
DR SMART; SM00406; 1g, 1.
FT NON_TER 1
FT 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 62.6%; Score 399.5; DB 4; Length 125;
Best Local Similarity 59.2%; Pred. No. 4.5e-35;
Matches 74; Conservative 21; Mismatches 25; Indels 5; Gaps 1;

QY 1 EVOLQSGAEIVKPGASVTKSCASGYTFNYFYWKORPGGLEWIGINRNDPTDF 60
Db 1 EVOLVESGAEIVKPGASVTKSCASGYTFGYMHVYRQAPGGGLEWIGINRSGSTV 60
QY 61 NEKFSRATITLVKSSSTAVMOJLSLTSEDSATYCTSPYGNNGFTYWGQGLTV 115
Db 61 AOKFGQVMTVTRDTSTVYMWELSLSESDTAVAYCARGSOGGRIRAAAGDAFIMGQGLTV 120
QY 116 TVSS 120
Db 121 TVSS 125

RESULT 12
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 20, 2001, 11:13:49 ; Search time 33.18 Seconds

(Without alignments)  
123.890 Million cell updates/sec

Title: US-09-615-872-1

Perfect score: 638  
Sequence: 1 EVQLQSGAEIVKRGASVKL.....YGNNGFTYWGCTIVTSA 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485	76.0	139	1	P01751 mus musculu
2	480.5	75.3	138	1	P03980 mus musculu
3	475.5	74.5	140	1	P01746 mus musculu
4	474.5	74.4	120	1	P01747 mus musculu
5	457	71.6	137	1	P01755 mus musculu
6	454.5	71.2	117	1	P01757 mus musculu
7	452	70.8	120	1	P06329 mus musculu
8	448.5	70.3	117	1	P01756 mus musculu
9	437	68.5	118	1	P06330 mus musculu
10	433	67.9	117	1	P01748 mus musculu
11	431	67.6	117	1	P06328 mus musculu
12	427.5	67.0	121	1	P01745 mus musculu
13	422	66.1	117	1	P01750 mus musculu
14	422	66.1	117	1	P01753 mus musculu
15	418	65.5	117	1	P01754 mus musculu
16	412	64.6	117	1	P01749 mus musculu
17	400	62.7	117	1	P06327 mus musculu
18	396	62.1	117	1	P01758 mus musculu
19	394.5	61.8	136	1	P01759 mus musculu
20	374	58.6	147	1	P01744 homo sapien
21	361	56.6	117	1	P01743 homo sapien
22	355	55.6	117	1	P23083 homo sapien
23	351	55.0	114	1	P01741 mus musculu
24	337	52.8	119	1	P01807 mus musculu
25	334	52.4	119	1	P01801 mus musculu
26	330.5	51.8	115	1	P01812 mus musculu
27	326.5	51.2	117	1	P01812 mus musculu
28	326	51.1	122	1	P01768 homo sapien
29	323.5	50.7	115	1	P01802 mus musculu
30	322.5	50.5	113	1	P01800 mus musculu
31	322.5	50.5	142	1	P01805 rattus norv
32	321.5	50.4	113	1	P01796 mus musculu
33	321.5	50.4	113	1	P01799 mus musculu

34	320.5	50.2	117	1	HV1A_HUMAN	P01742 homo sapien
35	319	50.0	120	1	HV1H_HUMAN	P80421 homo sapien
36	317	49.7	119	1	HV38_MOUSE	P01808 mus musculu
37	316	49.5	124	1	HV1D_HUMAN	P01760 homo sapien
38	315.5	49.5	113	1	HV28_MOUSE	P01797 mus musculu
39	313.5	49.1	113	1	HV29_MOUSE	P01798 mus musculu
40	312.5	49.0	121	1	HV3J_HUMAN	P01771 homo sapien
41	310.5	48.7	125	1	HV1E_HUMAN	P06326 homo sapien
42	305.5	47.9	117	1	HV4I_MOUSE	P01811 mus musculu
43	302.5	47.4	118	1	HV39_MOUSE	P01809 mus musculu
44	298	46.7	116	1	HV3T_HUMAN	P01781 homo sapien
45	297	46.6	111	1	HV35_MOUSE	P01804 mus musculu

## ALIGNMENTS

RESULT 1  
ID HV07\_MOUSE STANDARD: PRT: 139 AA.  
AC P01751, P01752; (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the Npb family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region."  
RL Cell 24:625-637(1981).  
CC -I- MISCELLANEOUS: THE BI-8 MG CHAIN mRNA WAS CLONED FROM A HYBRIDOMA  
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
CC (NPB ANTIBODIES).  
CC -----

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DR EMBL; J00529; AAA38170.1; -;  
DR PIR; A02034; MHMS18;  
DR InterPro; IPR003006; -;  
DR Pfam; PF00047; 19; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.  
FT DOMAIN 20 49 FRAMEWORK 1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 55 68 FRAMEWORK 2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 86 117 FRAMEWORK 3.  
FT DOMAIN 118 124 D SEGMENT.  
FT DOMAIN 125 139 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 139 139  
SQ SEQUENCE 139 AA; 15419 MM; 1B57DD4FD0C9F465 CRC64;

Query Match 76.0%; Score 485; DB 1; Length 139;  
Best Local Similarity 76.0%; Pred. No. 1; 1e-43;  
Matches 92; Conservative 16; Mismatches 11; Indels 2; Gaps 2;

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OY 1 EVOLQSGALVPGASVKLSCKASGYTFNFIYWKQKPGGGLGIGINPRNDTDF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 QVQLQPGALVPGASVKLSCKASGYTFNFIYWKQKPGGGLGIGINPRNDTDF 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NEKFSRATLTVDKSSSTAVMQLSLTSEDSATLYCTR-SPYGNNGFTYWGGLTVTS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NEKFSKATLTVDKPSSTAVMQLSLTSEDSAVYCARVDYSSY-FDYWGGLTVTS 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 A 120
DB 139 S 139

RESULT 2
HVA8_MOUSE
ID HV02_MOUSE STANDARD; PRT; 138 AA.
AC P01746;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HYMSG7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
OY 1 EVOLQSGALVPGASVKLSCKASGYTFNFIYWKQKPGGGLGIGINPRNDTDF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 QVQLQPGALVPGASVKLSCKASGYTFNFIYWKQKPGGGLGIGINPRNDGKSNY 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NEKFSRATLTVDKSSSTAVMQLSLTSEDSATLYCTRSP-YGNNGFTYWGGLTVTS 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NEKFSKATLTVDKSSSTAVMQLSLTSEDSAVYCARSD-GYDWMYVWGGLTVTS 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
HVA8_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 9367 PRECURSOR.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A/J;
RA MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
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DR EMBL: J00493; AAA38128.1; -.
DR PIR: A02028; HYMSG7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SO SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 74.5%; Score 475.5; DB 1; Length 140;
Best Local Similarity 75.2%; Pred. No. 1e-42;
Matches 91; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

OY 1 EVOLQSGALVPGASVKLSCKASGYTFNFIYWKQKPGGGLGIGINPRNDTDF 60
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DB 20 EVOLQSGALVPGASVKLSCKASGYTFNFIYWKQKPGGGLGIGINPRNDGKSNY 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NEKFSRATLTVDKSSSTAVMQLSLTSEDSATLYCTRSP-YGNNGFTYWGGLTVTS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NEKFSKATLTVDKSSSTAVMQLSLTSEDSAVYCARSHYGGSDFDYWGGLTVTS 139
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 A 120
DB 140 S 140

RESULT 4
HVA3_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=8331846; PubMed=6186498;
RA Stekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idioype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.

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DR PIR: A02028; HVM5G7.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; 19; 1.  
 KM Immunoglobulin V region; Antiarsonate antibody; Hydrindoma.  
 FT NON\_TER 120 120  
 SQ SEQUENCE 120 AA; 13307 MW; FF04EA167B654AF CRC64;

Query Match 74.4%; Score 474.5; DB 1; Length 120;  
 Best Local Similarity 75.8%; Pred. No. 1,1e-42;  
 Matches 91; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 2 VOLQOAGALVLRPGASVYKLSCKASGYTFYFYWKORPGGLEWIGELINPRNGDTDFN 61  
 DB 1 VOLQOAGALVLRPGASVYKLSCKASGYTFYFYWKORPGGLEWIGELINPRNGDTDFN 60  
 QY 62 EKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVTVSA 120  
 DB 61 EKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVTVSS 120

RESULT 5  
 HVL\_MOUSE  
 ID HVL\_MOUSE STANDARD; PRT; 137 AA.  
 AC P01755;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION S43 PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NpB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 CC (NPB ANTIBODIES).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL: J00539; AAA38172.1; -  
 DR PIR: A02038; G2MS43.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; 19; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT DOMAIN 118 122 D SEGMENT.  
 FT DOMAIN 123 137 JH2 SEGMENT.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 137 137  
 SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match

71.6%; Score 457; DB 1; Length 137;

Best Local Similarity 71.7%; Pred. No. 8.5e-41;  
 Matches 86; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

QY 1 EVOLQOAGALVLRPGASVYKLSCKASGYTFYFYWKORPGGLEWIGELINPRNGDTDF 60  
 DB 20 QVOLOQGAELVLRPGASVYKLSCKASGYTFYFYWKORPGGLEWIGELINPRNGDTDF 79  
 QY 61 NEKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVTVSA 120  
 DB 80 NEKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVTVSS 137

RESULT 6  
 HVL\_MOUSE  
 ID HVL\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01757;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION J558.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=80078170; PubMed=6765983;  
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;  
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
 RT rearrangements in heavy chain V-region gene segments.";  
 RL Nature 283:35-40(1980).  
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO  
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF  
 CC WHICH OCCUR IN THE D AND J SEGMENTS.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
 CC PIR: A26242; MEMSJS.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; 19; 1.  
 KM Immunoglobulin V region.  
 FT DISULFID 22 96 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 71.2%; Score 454.5; DB 1; Length 117;  
 Best Local Similarity 71.7%; Pred. No. 1.3e-40;  
 Matches 86; Conservative 14; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVOLQOAGALVLRPGASVYKLSCKASGYTFYFYWKORPGGLEWIGELINPRNGDTDF 60  
 DB 1 EVOLQOAGALVLRPGASVYKLSCKASGYTFYFYWKORPGGLEWIGELINPRNGDTDF 60  
 QY 61 NEKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVTVSA 120  
 DB 61 NEKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVTVSS 117

RESULT 7  
 HVL\_MOUSE  
 ID HVL\_MOUSE STANDARD; PRT; 120 AA.  
 AC P06329;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION AC38 15.3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=84182519; PubMed=6201362;  
 RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

RT	"A V region determinant (idiotope) expressed at high frequency in B			
RT	lymphocytes is encoded by a large set of antibody structural genes."			
RL	EMBO J. 3:517-523(1984).			
DR	PIR: A02037; MHMS15.			
DR	InterPro: IPR003006; -.			
DR	Pfam: PF00047; Ig; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN	1	98	V SEGMENT.
FT	DOMAIN	99	105	D SEGMENT.
FT	DOMAIN	106	120	J SEGMENT.
FT	DISULFID	22	96	BY SIMILARITY.
FT	NON TER	120	120	
SQ	SEQUENCE	120 AA;	13311 MW;	914453F426F09834 CRCC4;

Query Match	70.8%	Score 453	DB 1	Length 120
Best Local Similarity	70.0%	Pred. NO. 2.4e-40		
Matches 84	Conservative 15	Mismatches 21	Indels 0	Gaps 0

Qy	1	EVQLQDSAEELVKKRGASVKISCKKASGTFYFVWKQKPGQGLIEWIGELINPENGDTDF	60
		:     :     :     :     :     :     :     :     :     :	
Db	1	QVQLDPTGTELVKRGASVNIISKASGTFYFVWMMHMLRQKPGQGLIEWIGELINPENGSTNY	60
		:     :     :     :     :     :     :     :     :	
Qy	61	NEKEESRATILVYDKSSSTAYHWQLSSLSIEDSAYITCYTRSPFGANNYGTYYGGTGLVTVSA	120
		:     :     :     :     :     :     :     :     :	
Db	61	NEKRSKATILVYDKSSSAYHWQLSSLSIEDSAYVYCARMDYEGRIYVDWGGTGLVTVSS	120
		:     :     :     :     :     :     :     :     :	

	Query Match	70.3%	Score 448.5:	DB 1,	Length 117,
	Best Local Similarity	70.8%:	Pred. No. 5.4e-40;		
	Matches	85;	Conservative 15;	Mismatches 17;	Gaps 3;
Qy	1	EVLQOOGAEIVKPGASVYKLSCKRAGSYTFNNFYVWKORPQGLIEWELINPRNGTDF	60		
Dd	1	EVLQOOGPELVKPGASVYKMSCKRASGITFTDYIKWVKQSHGKSLEWIGINPNRGSTGY	60		
Qy	61	NKKESRATLTVDKSSSTAAMQLSLTSSESAIYTCRRSPYGNNYGGTYMGCGILVYSA	120		
		:   :			
Dd	61	NKKKGATLTVDKSSSTAAMQLSLTSSESAIYTCARD--YDMVFDMGACTTYYVSS	117		

RL	EMBO J. 3:517-523(1984).	
DR	PIR: A02040; MHMS38.	
DR	InterPro: IPR003006; -.	
DR	Pfam: PF00047; 1g; 1.	
KW	Immunoglobulin V region.	
DOMAIN	1	
FT	98	V SEGMENT.
FT	104	D SEGMENT.
FT		

Query Match	67.68;	Score 431;	DB 1;	Length 117;
Best Local Similarity	82.58;	Pred. NO. 3.6e-38;		
Matches 80;	Conservative 11;	Mismatches 6;	Indels 0;	Gaps 0;

RESULT	13
HV06_MOUSE	
ID	
AC	21-JUL-1986 (rel. 01, Created)
DT	21-JUL-1986 (rel. 01, Last sequence update)
DT	15-JUL-1999 (rel. 38, Last annotation update)
DE	IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
OX	NBRL_TaxID=10090;
RP	[1] SEQUENCE FROM N.A.

RC STRAIN-C57BL/6;  
RX MEDLINE-81234548; PubMed-6788376;  
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K., Baltimore D.;  
RT "heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
DR A02032; HWS02.  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; 1g; 1.  
KW Immunoglobulin V region; Signal.  
FT CHAIN 1 19  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.  
FT DOMAIN 20 49 FRAMEWORK 1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 55 68 FRAMEWORK 2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 86 117 FRAMEWORK 3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FC8C CRC64;

Query Match 66.1%; Score 422; DB 1; Length 117;  
Best Local Similarity 81.1%; Pred. No. 3.1e-37;  
Matches 77; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY 2 VOLOQSGAEIVKPGASVKLSCKASGYTFYTWVKORPGGLEWIGELINPRNGDTDF 61  
DB 21 VOLOQSGAEIVKPGASVKLSCKASGYTFYTWVKORPGGLEWIGELINPRNGDTDF 80  
QY 62 EKFSRATITVDKSSSTAYWQLSLTSEDSAYVYC 96  
DB 81 QKFKKATITVDKSSSTAYWQLSLTSEDSAYVYC 115

RESULT 14  
ID HV09\_MOUSE STANDARD; PRT; 117 AA.  
HV09\_MOUSE  
AC P01753; P11271;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6;  
RX MEDLINE-81234548; PubMed-6788376;  
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K., Baltimore D.;  
RT "heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
DR A02032; HWS01.  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; 1g; 1.  
KW Immunoglobulin V region; Signal.  
FT CHAIN 1 19  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.  
FT DOMAIN 20 49 FRAMEWORK 1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 55 68 FRAMEWORK 2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 86 117 FRAMEWORK 3.  
FT DISULFID 41 115 BY SIMILARITY.

FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 66.1%; Score 422; DB 1; Length 117;  
Best Local Similarity 79.6%; Pred. No. 3.1e-37;  
Matches 78; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVOLQSGAEIVKPGASVKLSCKASGYTFYTWVKORPGGLEWIGELINPRNGDTDF 60  
DB 20 EVOLQSGAEIVKPGASVKLSCKASGYTFYTWVKORPGGLEWIGELINPRNGDTDF 79  
QY 61 NEKFSRATITVDKSSSTAYWQLSLTSEDSAYVYC 98  
DB 80 NEKFSRATITVDKSSSTAYWQLSLTSEDSAYVYC 117

RESULT 15  
ID HV10\_MOUSE STANDARD; PRT; 117 AA.  
HV10\_MOUSE  
AC P01754; P11270;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V REGION 145 PRECURSOR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6;  
RX MEDLINE-81234548; PubMed-6788376;  
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K., Baltimore D.;  
RT "heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; J00533; AAA38602.1; -  
DR PIR; C02034; HWS45.  
DR InterPro: IPR003006; -  
DR Pfam: PF00047; 1g; 1.  
KW Immunoglobulin V region; Signal.  
FT CHAIN 1 19  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.  
FT DOMAIN 20 49 FRAMEWORK 1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 55 68 FRAMEWORK 2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 86 117 FRAMEWORK 3.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 65.5%; Score 418; DB 1; Length 117;  
Best Local Similarity 79.6%; Pred. No. 8.1e-37;  
Matches 78; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVOLQSGAEIVKPGASVKLSCKASGYTFYTWVKORPGGLEWIGELINPRNGDTDF 60  
DB 20 EVOLQSGAEIVKPGASVKLSCKASGYTFYTWVKORPGGLEWIGELINPRNGDTDF 79

Thu Jun 21 10:32:46 2001

us-09-615-872-1.rsp

Page 7

```

Qy      61 NEKESRATLTVDKSSSTAYMQLSLTSEDAIYYCTR  98
        |||:::||||| |||||||||:::|
Db      80 NEKFSKATLTVDKPSTAYMQLSLTSEDAVYYCAR  117

```

Search completed: June 20, 2001, 11:18:56  
Job time: 307 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 20, 2001, 10:47:39 ; Search time 61.83 Seconds

(without alignments)  
147.840 Million cell updates/sec

Title: US-09-615-872-1

Perfect score: 638

Sequence: 1 EVQLQSGAEELVKPGASVKL.....YGNNGFTYWGQGLTVTVSA 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: PIR-68:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509.5	79.9	116	2 S55542	Ig heavy chain V r
2	498.5	78.1	138	2 S21810	Ig heavy chain V r
3	492	77.1	120	2 S41394	Ig heavy chain V r
4	486	76.2	126	2 S31930	Ig gamma chain pre
5	485	76.0	139	1 MHMS18	Ig heavy chain pre
6	483	75.7	118	2 PC4402	pe1b leader/Ig hea
7	483	75.7	139	2 C30560	Ig heavy chain V r
8	483	75.7	139	2 PS0024	Ig heavy chain pre
9	482.5	75.6	131	2 A27472	Ig heavy chain pre
10	481	75.3	120	2 B22769	Ig heavy chain V r
11	480.5	75.3	138	1 HVMST7	Ig heavy chain pre
12	479.5	75.2	140	2 PH1482	Ig heavy chain V r
13	477	74.8	135	2 A30577	Ig heavy chain pre
14	476.5	74.7	119	2 C30562	Ig heavy chain pre
15	475.5	74.5	140	1 HVMST7	Ig heavy chain V r
16	474.5	74.4	119	2 E30562	Ig heavy chain V r
17	473.5	74.2	117	2 JC2269	Ig heavy chain pre
18	471.5	73.9	120	2 S25175	pl7-6 antibody hea
19	471.5	73.9	123	2 S20646	Ig heavy chain V r
20	471.5	73.9	138	2 E32513	Ig heavy chain pre
21	471	73.8	141	2 JL0076	Ig heavy chain pre
22	469.5	73.6	121	2 A26405	Ig heavy chain V r
23	469	73.5	115	2 A54378	Ig heavy chain V r
24	469	73.5	117	2 S25176	Ig heavy chain V r
25	467.5	73.3	119	2 D30562	Ig heavy chain V r
26	467	73.2	123	2 S60067	Ig heavy chain V r
27	467	73.2	137	2 E29380	Ig heavy chain pre
28	466.5	73.1	118	2 S38565	Ig heavy chain V r
29	465.5	73.0	119	2 S20640	Ig heavy chain V r

30	465.5	73.0	246	2 S38950	Ig gamma chain - m
31	465.5	73.0	46	2 S40295	Ig gamma-2a chain
32	464.5	72.8	136	2 PL0208	Ig heavy chain pre
33	462.5	72.5	122	2 S20643	Ig heavy chain V r
34	462.5	72.5	135	2 PH1493	Ig heavy chain V r
35	462.5	72.5	140	2 PH1484	Ig heavy chain V r
36	462	72.4	116	2 S53751	antibody Fab Jel 1
37	462	72.4	117	2 B27563	Ig heavy chain V r
38	462	72.4	136	2 JL0077	Ig heavy chain pre
39	461	72.3	113	2 S25041	Ig heavy chain V r
40	461	72.3	135	2 PS0057	Ig heavy chain pre
41	461	72.3	137	2 F29380	Ig heavy chain pre
42	461	72.3	139	2 A27609	Ig heavy chain pre
43	460.5	72.2	125	2 S20639	Ig heavy chain V r
44	460.5	72.2	140	2 PH1489	Ig heavy chain V r
45	460	72.1	113	2 S25044	Ig heavy chain V r

## ALIGNMENTS

```
RESULT 1
S55542
Ig heavy chain V region pe2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies u
utations in the variable region genes.
A:Reference number: S55528; MWID:95239763
A:Accession: S55542
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <BOE>
A:Cross-references: EMBL:X82581; NID:9854302; PIDN:CAA57917.1; PID:9854303
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:14-97/Domain: Immunoglobulin homology <IMM>

Query Match 79.9%; Score 509.5; DB 2; Length 116;
Best Local Similarity 82.4%; Pred. No. 1,1e-39;
Matches 98; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 2 VOLQSGAEELVKPGASVKLSCKASGYTFYTWKQRPQGLEWIGELINPRNGDTDFN 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 VOLQSGAEELVKPGASVKLSCKASGYTFYTWKQRPQGLEWIGELINPRNGDTDFN 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 EKESRATLVDRKSSSTAYVQSLTSEDAITTCRSPYGNNGFTYWGQGLTVTVSA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EKESRATLVDRKSSSTAYVQSLTSEDAITTCRSPYGNNGFTYWGQGLTVTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
S21810
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
R:Stemeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy
A:Reference number: S21810
A:Accession: S21810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <OST>
A:Cross-references: EMBL:X56936; NID:954163; PIDN:CAA40257.1; PID:954164
C:Genetics:
A:Introns: 15/3
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
```





```

RESULT      8
PS0024
Ig heavy chain precursor V region (6A4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C/Accession: PS0024
R:Merger, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Ember 74, 335-345, 1988

```

RESULT 10  
B22769  
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Dec-1987 #sequence-revision 28-Dec-1987 #text-change 16-Aug-1996  
C:Accession: B22769  
R:Dildrop, R.; Brugemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.  
EMBO J. 1, 635-640, 1982  
#:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between





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OM protein - protein search, using sw model

Run on: June 20, 2001, 10:47:39 ; Search time 29.71 Seconds

(without alignments)  
81.365 Million cell updates/sec

Title: US-09-615-872-1

Perfect score: 638

Sequence: 1.EVQLQQSGAEIVKPGASVKL.....YGNNGFTYWGQTLVTVA 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515.5	80.8	116	US-08-737-560A-7	Sequence 7, Appl
2	507.5	79.5	119	US-08-553-497A-12	Sequence 12, Appl
3	506.5	79.4	119	US-08-737-560A-10	Sequence 10, Appl
4	501	78.5	122	US-08-236-520-9	Sequence 9, Appl
5	501	78.5	122	PCT-US95-05262-9	Sequence 9, Appl
6	500.5	78.4	139	US-08-894-922A-5	Sequence 5, Appl
7	500.5	78.4	252	US-08-894-922A-14	Sequence 14, Appl
8	500.5	78.4	271	US-08-894-922A-10	Sequence 10, Appl
9	495.5	77.7	123	US-08-497-312-15	Sequence 15, Appl
10	495.5	77.7	123	US-08-560-558E-28	Sequence 28, Appl
11	493.5	77.4	143	US-08-236-520-7	Sequence 7, Appl
12	493.5	77.4	143	PCT-US95-05262-7	Sequence 7, Appl
13	490.5	76.9	445	US-08-353-400-33	Sequence 33, Appl
14	490.5	76.9	464	US-08-353-400-36	Sequence 36, Appl
15	489	76.6	120	US-08-397-411-11	Sequence 11, Appl
16	489	76.6	139	US-08-656-586-4	Sequence 4, Appl
17	488.5	76.6	244	US-08-553-497A-20	Sequence 20, Appl
18	488.5	76.6	246	US-08-553-497A-24	Sequence 24, Appl
19	488	76.5	269	US-08-428-257A-72	Sequence 72, Appl
20	488	76.5	269	US-08-491-988-3	Sequence 3, Appl
21	488	76.5	402	US-08-491-988-9	Sequence 9, Appl
22	488	76.5	415	US-08-491-988-7	Sequence 7, Appl
23	488	76.5	435	US-08-403-853-18	Sequence 5, Appl
24	486	76.2	273	US-08-403-853-18	Sequence 18, Appl
25	485.5	76.1	119	US-08-553-497A-8	Sequence 8, Appl
26	483	75.7	128	US-08-202-047-21	Sequence 21, Appl
27	483	75.7	128	US-08-964-690-21	Sequence 21, Appl

28	482.5	75.6	244	2	US-08-553-497A-22	Sequence 22, Appl
29	479	75.1	115	2	US-08-672-345C-18	Sequence 18, Appl
30	479	75.1	115	2	US-08-672-345C-108	Sequence 108, Appl
31	477.5	74.8	119	4	US-08-767-128-10	Sequence 10, Appl
32	477.5	74.8	140	1	US-07-946-421-24	Sequence 24, Appl
33	477.5	74.8	242	2	US-08-553-497A-76	Sequence 26, Appl
34	476.5	74.7	119	4	US-08-767-128-6	Sequence 6, Appl
35	476.5	74.7	123	1	US-08-497-312-17	Sequence 17, Appl
36	474.5	74.4	138	1	US-08-482-882-78	Sequence 78, Appl
37	474.5	74.4	138	2	US-08-483-389-78	Sequence 78, Appl
38	474.5	74.4	138	2	US-08-487-113D-78	Sequence 78, Appl
39	474.5	74.4	138	2	US-08-473-503-78	Sequence 78, Appl
40	474.5	74.4	138	2	US-08-483-932-78	Sequence 78, Appl
41	474.5	74.4	138	2	US-08-720-430A-78	Sequence 78, Appl
42	474.5	74.4	138	3	US-08-714-017-78	Sequence 78, Appl
43	474.5	74.4	138	3	US-08-475-680-78	Sequence 78, Appl
44	473	74.1	117	3	US-09-065-059-15	Sequence 15, Appl
45	473	74.1	119	1	US-08-467-393-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-737-560A-7  
Sequence 7, Application US/08737560A  
Patent No. 592893  
GENERAL INFORMATION:  
APPLICANT: KANG, Chang-Yuill  
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESS: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
SREET: Kwanak-gu  
CITY: Seoul  
STATE: Seoul  
COUNTRY: Republic of Korea  
ZIP: 151-057  
ADDRESS: KIM, Joong-Gon  
SREET: Hanyang Apt. 72-1213, Apgu Jung-dong, Kangnam-gu  
CITY: Seoul  
STATE: Seoul  
COUNTRY: Republic of Korea  
ZIP: 135-110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
COMPUTER: IBM PC/AT  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/737,560A  
FILING DATE: 13-NOV-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: KR 95-8176  
FILING DATE: 08-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:









TELEFAX: (202)-822-0944  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 271 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-894-922a-10

Query Match 78.4%; Score 500.5; DB 2; Length 271;  
 Best Local Similarity 80.8%; Pred. No. 1.5e-42;  
 Matches 97; Conservative 11; Mismatches 9; Indels 3; Gaps 2;

OY 1 EVOLQOSGALVPRGASVKSCKASGTFNTNYFYWKORPGGLEWIGINPRNGDTDF 60  
 :|||||  
 DB 23 QVLOQOSGALVPRGASVKSCKASGTFNTNYFYWKORPGGLEWIGINPTSGSNF 82  
 :|||||  
 OY 61 NEKFESRATLVDSSTAVAMOLSLTSEDSAYYCTRSFYGNNYGTWGGTTLVT 120  
 :|||||  
 DB 83 NEKFATKATLVDSSTAVAMOLSLTSEDSAYYCTRCGLWPFDSGRCDFMGQGTTLT 139  
 :|||||

RESULT 9  
 US-08-497-312-15  
 ; Sequence 15, Application US/08497312  
 ; Patent No. 5712120  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Method for obtaining modified  
 ; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR  
 ; STREET: 215 Y 15, ATABEY PLAYA  
 ; CITY: HAVANA  
 ; STATE:  
 ; COUNTRY: CUBA  
 ; ZIP: 11600  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/497,312  
 ; FILING DATE: 30-JUN-1995  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: CU 80/94  
 ; FILING DATE: 30-JUN-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BOND, LAURENCE B.  
 ; REGISTRATION NUMBER: 30,549  
 ; REFERENCE/DOCKET NUMBER: 2629US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 801/532-1922  
 ; TELEFAX: 801/531-9168  
 ; TELEX: 388961 JPMOJUT  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 123 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; US-08-497-312-15

Query Match 77.7%; Score 495.5; DB 1; Length 123;  
 Best Local Similarity 75.6%; Pred. No. 1.9e-42;  
 Matches 93; Conservative 15; Mismatches 12; Indels 3; Gaps 1;

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 DB 1 QVLOQOSGALVPRGASVKSCKASGTFNTNYFYWKORPGGLEWIGINPTSGSNF 60  
 :|||||  
 OY 61 NEKFESRATLVDSSTAVAMOLSLTSEDSAYYCTRSFYGNNYGTWGGTTLVT 117  
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 DB 61 NEKFATKATLVDSSTAVAMOLSLTSEDSAYYCTRCGLWPFDSGRCDFMGQGTTLT 120  
 :|||||

OY 118 VSA 120  
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 DB 121 VSS 123

RESULT 10  
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 ; Sequence 28, Application US/08560558E  
 ; Patent No. 5891996  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Humanized and chimeric monoclonal  
 ; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA  
 ; STREET: P.O. Box 2250  
 ; CITY: Salt Lake City  
 ; STATE: Utah  
 ; COUNTRY: United States of America  
 ; ZIP: 84110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: WINDOWS95  
 ; SOFTWARE: Wordperfect 5.1/5.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/560,558E  
 ; FILING DATE: NO. 5891996ember 17, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Turner, Allen C.  
 ; REGISTRATION NUMBER: 33,041  
 ; REFERENCE/DOCKET NUMBER: 2720US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (801) 531-9168  
 ; TELEFAX: (801) 531-9168  
 ; INFORMATION FOR SEQ ID NO: 28:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 123 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; US-08-560-558E-28

Query Match 77.7%; Score 495.5; DB 2; Length 123;  
 Best Local Similarity 75.6%; Pred. No. 1.9e-42;  
 Matches 93; Conservative 15; Mismatches 12; Indels 3; Gaps 1;

OY 1 EVOLQOSGALVPRGASVKSCKASGTFNTNYFYWKORPGGLEWIGINPRNGDTDF 60  
 :|||||  
 DB 1 QVLOQOSGALVPRGASVKSCKASGTFNTNYFYWKORPGGLEWIGINPTSGSNF 60  
 :|||||  
 OY 61 NEKFESRATLVDSSTAVAMOLSLTSEDSAYYCTRSFYGNNYGTWGGTTLVT 117  
 :|||||  
 DB 61 NEKFATKATLVDSSTAVAMOLSLTSEDSAYYCTRCGLWPFDSGRCDFMGQGTTLT 120  
 :|||||

OY 118 VSA 120  
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 DB 121 VSS 123

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1 COUNTRY: USA
2 ZIP: 02173
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: Patentin Release #1.0, Version #1.25
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: PCT/US95/05262
11 FILING DATE:
12 CLASSIFICATION:
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: U.S. 08/236,520
15 FILING DATE: April 29, 1994
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Granahan, Patricia
18 REGISTRATION NUMBER: 27,227
19 REFERENCE/DOCKET INFORMATION:
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 617-861-9540
22 TELEFAX: 617-861-6240
23 INFORMATION FOR SEQ ID NO: 7:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 143 amino acids
26 TYPE: amino acid
27 TOPOLOGY: linear
28 MOLECULE TYPE: protein
29 PCT-US95-05262-7
30
31 Query Match 77.4%, Score 493.5, DB 5; Length 143:
32 Best Local Similarity 76.9%, Pred. No. 3,6e-42;
33 Matches 93; Conservative 14; Mismatches 13; Indels 1; Gaps 14.
34
35 Oy 1 EVOLQSGAEVLKPPASVYKLSCKAGSYFTNFYIYWKVKORPGGLEWIEINPRNGDTDF 60
36 Db 20 OVQLOQPGTELKPPASVYKLSCKAGSYFTTFYIYWKVKORPGGLEWIEINIPNSGCTNY 79
37 Oy 61 NEKEFSRATLVYDKSSSTAYWOLSSLTSEDSAI-YYCTRSPPYGNNGFTYYWGCGTLVYS 119
38 Db 80 NEKEFSKATLVYDKSSSTAYWOLSSLTSEDSAAVYVYARRAPYGGSRNPDYWGCGTLTVS 139
39 Oy 120 A 120
40 Db 140 S 140
41
42 RESULT 13
43 US-08-353-400-33
44 Sequence 33, Application US/08353400
45 Patent No. 5665357
46 GENERAL INFORMATION:
47 APPLICANT:
48 TITLE OF INVENTION: PROTEINS
49 NUMBER OF SEQUENCES: 37
50 COMPUTER READABLE FORM:
51 MEDIUM TYPE: Floppy disk
52 COMPUTER: IBM PC compatible
53 OPERATING SYSTEM: PC-DOS/MS-DOS
54 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
55 CURRENT APPLICATION DATA:
56 APPLICATION NUMBER: US/08/353,400
57 FILING DATE:
58 CLASSIFICATION: 424
59 PRIOR APPLICATION DATA:
60 APPLICATION NUMBER: GB 9324819.3
61 FILING DATE: 03-DEC-1993
62 PRIOR APPLICATION DATA:
63 APPLICATION NUMBER: GB 9411089.7
64 FILING DATE: 03-JUN-1994
65 INFORMATION FOR SEQ ID NO: 33:
66 SEQUENCE CHARACTERISTICS:
67 LENGTH: 445 amino acids

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Page 7

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60120  
120

0;

60  
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120



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 10:47:39 ; Search time 66.12 seconds

(without alignments)  
103.745 Million cell updates/sec

Title: US-09-615-872-1

Perfect score: 638

Sequence: 1 EVQLQSGAEIVKRGASVKL.....YGNNGFTYWGQGLTVTSA 120

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	511	80.1	256	13	R22568	ScFvB18 construct.
2	511	80.1	256	13	R22582	ScFvB18 construct.
3	511	80.1	256	13	R22583	ScFvB18 construct.
4	511	80.1	256	13	R22584	ScFvB18 construct.
5	511	80.1	256	13	R22585	ScFvB18 construct.
6	511	80.1	256	13	R22586	ScFvB18 construct.
7	511	80.1	256	13	R22587	ScFvB18 construct.
8	507.5	79.5	119	16	R79863	Anti-EGFR antibody
9	506.5	79.4	119	17	W04332	Heavy chain of mon
10	501	78.5	122	16	R84555	B-cell lymphoma CH
11	500.5	78.4	119	21	V71473	Mouse monoclonal a

12	500.5	78.4	139	17	W02291	FWC-II VH region.
13	500.5	78.4	252	17	W02294	Yeast-FWC-II-KEX2
14	500.5	78.4	271	17	W02293	FWC-II-KEX2. Chl
15	497.5	78.0	136	8	P70624	Sequence encoded b
16	497.5	78.0	136	8	W10564	Anti-hepatitis B h
17	497.5	78.0	136	18	W16340	Mouse-human chimae
18	497.5	78.0	136	18	W10239	Chimeric anti-hepa
19	497.5	78.0	136	19	W47510	Human anti-hepatit
20	497.5	78.0	136	19	W41054	Human anti-hepatit
21	497.5	78.0	136	19	W47517	Human anti-hepatit
22	497.5	78.0	136	20	W89535	Human anti-hepatit
23	495.5	77.7	123	17	R92990	Chimeric anti-hepa
24	493.5	77.4	143	16	R84554	Monoclonal antibod
25	493	77.3	428	18	W24027	Mb SCH94.03 heavy
26	493	77.3	443	18	W24025	Single chain antiq
27	491.5	77.0	288	20	W62743	Single chain antiq
28	491.5	77.0	673	20	W62742	Fusion protein PNG
29	490.5	76.9	445	16	R76085	Plasmid PNG4/55.1s
30	490.5	76.9	464	16	R76088	Mb 55.1 heavy cha
31	489.5	76.7	117	17	R88716	Mouse antibody hea
32	489	76.6	139	19	W36167	Heavy chain variab
33	488.5	76.6	244	16	R79867	Anti-EGFR single c
34	488.5	76.6	244	16	R79873	Anti-EGFR single c
35	488.5	76.6	246	16	R79869	Anti-EGFR single c
36	488	76.5	269	15	R54756	PRAS11 between H1
37	488	76.5	269	15	R56482	ScFv PRAS107 and p
38	488	76.5	402	15	R56485	ScFv PRAS107 and p
39	488	76.5	435	15	R56483	ScFv PRAS108 and p
40	486	76.2	273	15	R52865	Anti-Influenza N10
41	485.5	76.1	119	16	R79861	Anti-EGFR antibody
42	484.5	75.9	242	16	R79872	Anti-EGFR single c
43	484	75.9	415	15	R56484	ScFv PRAS109 and p
44	483.5	75.8	121	16	R74964	Anti-Idiotypic anti
45	483	75.7	159	10	P93079	Heavy chain of mon

# ALIGNMENTS

RESULT 1	
ID R22568	standard; Protein: 256 AA.
AC R22568;	
XX 21-MAY-1992 (first entry)	
XX ScFvB18 construct.	
DE Fd: bacteriophage; gene III: filamentous; phagemid; capsid; coat;	
XX plus: g3p: binding; adsorption; gene VIII: diverse repertoire;	
KW specific binding pairs; replicable genetic display package.	
KW Synthetic.	
XX OS	
XX Key	Location/Qualifiers
FT Misc-difference 103	/label= mutation
FT FT	/note= Ala -> Val (VH FR3) x 3 "
FT FT	/label= mutation
FT FT	/note= Tyr -> Asp (VL CDR3) x 1 "
FT FT	/label= mutation
FT FT	/note= Ser -> Gly (VL CDR3) x 1 "
FT FT	/label= mutation
FT FT	/note= Gly -> Ser (VL FR4) x 21; or
FT FT	Gly -> Asp (VL FR4) x 3 "
FT FT	/label= mutation
FT FT	/note= Thr -> Ile (VL FR4) x 1 "

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PN W09201047-A.
XX
PD 23-JAN-1992.
XX
PE 10-JUL-1991; 91WO-GB01134.
XX
PR 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
PA (CMB-) CAMBRIDGE ANTIBODY.
PA (MED-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD,
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;
XX
DR WPI: 1992-056862/07.
DR N-PSDB; Q21100.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 38; Fig 44; 209pp; English.
XX
CC The sequence is encoded by an antibody scfv fragment directed
CC against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
CC an MAb against NP were separately amplified and reassembled to form
CC the construct, which was then ligated into the fd gene III contg.
CC vector, fdCAT2, derived from fdmps/Xh. (See Q21095). The clone having
CC the scfvB18 sequence fused in frame to gene III was designated
CC fdCAT2scfvB18. Alternatively the fragment was cloned into fdDOGkan
CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC to give fdDOGkanscfvB18, or into the phagemid PHEM1 to create PHEM1-
CC scfvB18. The constructs were used to test the effect of using muta-
CC tor strains to increase the diversity of the cloned genes. The
CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
CC mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
CC mutation and screening, 40 phage inserts were sequenced. They each
CC displayed single mutations in 6 different positions, five being in
CC the light chain region. More than 70% of the mutations occurred at
CC positions 724 and 725 (of the nucleotide sequence) changing the
CC first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
CC (in 3 cases). The mutant fragments had affinities for NP which were
CC comparable to the wild-type scfv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also R21260-307, 309-311; R22450, 565-581.
XX
SQ Sequence 256 AA;

```

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Query Match 80.1%; Score 511; DB 13; Length 256;
Best Local Similarity 78.3%; Pred. No. 1,7e-37;
Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

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Db 7 qvqdgqgaeeivkpgasvrlscasgyftfymhwkvqgrgrglewgridpmsgqtky 66
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 61 NEKESRATLTVDKSSSTAYWQSLTSLSAIIYCTRSPYGNNGYFTYWGQGLVTYVSA 120
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 67 nekfskattlvdkpsstaywqsltslsedaayycarydyssyfydwgqgtvtvss 126
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RESULT 2
R22582
ID R22582 standard; Protein; 256 AA.
XX
AC R22582;
XX

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DT 21-MAY-1992 (first entry)
DE
XX ScfvB18 construct mutant #1.
XX
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT Misc-difference 103
FT /label= mutation
FT /note=" Ala -> Val (VH FR3) "
XX
PN W09201047-A.
XX
PD 23-JAN-1992.
XX
PE 10-JUL-1991; 91WO-GB01134.
XX
PR 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
PA (CMB-) CAMBRIDGE ANTIBODY.
PA (MED-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;
XX
DR WPI: 1992-056862/07.
DR N-PSDB; Q23858.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 38; Fig 44; 209pp; English.
XX
CC The sequence is encoded by an antibody scfv fragment directed
CC against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
CC an MAb against NP were separately amplified and reassembled to form
CC the construct, which was then ligated into the fd gene III contg.
CC vector, fdCAT2, derived from fdmps/Xh. (See Q21095). The clone having
CC the scfvB18 sequence fused in frame to gene III was designated
CC fdCAT2scfvB18. Alternatively the fragment was cloned into fdDOGkan
CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC to give fdDOGkanscfvB18, or into the phagemid PHEM1 to create PHEM1-
CC scfvB18. The constructs were used to test the effect of using muta-
CC tor strains to increase the diversity of the cloned genes. The
CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
CC mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
CC mutation and screening, 40 phage inserts were sequenced. They each
CC displayed single mutations in 6 different positions, five being in
CC the light chain region. More than 70% of the mutations occurred at
CC positions 724 and 725 (of the nucleotide sequence) changing the
CC first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
CC (in 3 cases). The mutant shown here occurred three times. The
CC mutant fragments had affinities for NP which were comparable to the
CC wild-type scfv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also R21260-307, 309-311; R22450, 565-581.
XX
SQ Sequence 256 AA;

```

```

Query Match 80.1%; Score 511; DB 13; Length 256;
Best Local Similarity 78.3%; Pred. No. 1,7e-37;
Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

```

```

OY      1  EVOLOOGSAELVKGASVRLSKKASGYTFNFYIYWKORPGGLEWIGELINPBGDTDF 60
       :|||||
Db      7  qvdlqsgaelvkgasvrlskkasytlftsymhwkqrpgrglewigrldpnsqgltky 66
       :|||||
OY      61 NEKFESRALTVDKSSSTAYMQLSLTSEDSAIYCTRSPYGNNGFTYWGQGLTVTVA 120
       :|||||
Db      67 nekfkakltvdkpsstaymqjssltssedsavycarydygssyfdywgqglvtvts 126

RESULT  3
R22583  R22583 standard; Protein: 256 AA.
XX
AC      R22583;
XX
DT      21-MAY-1992 (first entry)
XX
DE      scfVb18 construct #2.
XX
KM      fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KM      plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KM      specific binding pairs; replicable genetic display package.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 235      /label= mutation
FT      /note=" Tyr -> Asp (VL CDR3) "
XX
PN      MO9201047-A.
XX
PD      23-JAN-1992.
XX
PF      10-JUL-1991; 91WO-GB01134.
XX
PR      15-MAY-1991; 91GB-0010549.
PR      10-JUL-1990; 90GB-0015198.
PR      19-OCT-1990; 90GB-0022845.
PR      12-NOV-1990; 90GB-0024503.
PR      06-MAR-1991; 91GB-0004744.
XX
PA      (CAMB-) CAMBRIDGE ANTIBODY.
XX      (MED-) MED RES COUNCIL.
XX
PI      McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI      Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI      Winter GP, Bonnett TP;
XX
DR      WPI: 1992-056862/07.
DR      N-PSDB; Q23859.
XX
PT      Producing members of specific binding pairs - by expression in
PT      recombinant host cells with a secreting replicable genetic
PT      display package.
XX
PS      Example 38; Fig 44; 209pp; English.
XX
CC      The sequence is encoded by an antibody scfv fragment directed
CC      against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
CC      an Mab against NP were separately amplified and reassembled to form
CC      the construct, which was then ligated into the fd gene III contg.
CC      vector, fdCAT2, derived from fdmps/Xh. (See Q21095). The clone having
CC      the scfVb18 sequence fused in frame to gene III was designated
CC      fdCAT2scfVb18. Alternatively the fragment was cloned into fdDOCKan
CC      (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC      to give fdDOCKanscfVb18, or into the phagemid pHEM1 to create pHEM1-
CC      scfVb18. The constructs were used to test the effect of using muta-
CC      tor strains to increase the diversity of the cloned genes. The
CC      strains NR9046mut5: NR9046 mutD5::Tn10 and NR9046mut1: NR9046
CC      mut1::Tn10 were constructed by P1 transduction. After 4 rounds of
CC      mutation and screening, 40 phage inserts were sequenced. They each

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```

CC      displayed single mutations in 6 different positions, five being in
CC      the light chain region. More than 70% of the mutations occurred at
CC      positions 724 and 725 (of the nucleotide sequence) changing the
CC      first Gln in the J segment (framework 4) to Ser (in 21 cases) or Asp
CC      (in 3 cases). The mutant shown here occurred once. The mutant frag-
CC      ments had affinities for NP which were comparable to the wild-type
CC      scfv fragment (20nM).
CC      N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC      See also R21260-307, 309-311; R22450, 565-581.
XX
SQ      Sequence      256 AA;

Query Match      80.1%; Score 511; DB 13; Length 256;
Best Local Similarity 78.3%; Pred. No. 1.7e-37;
Matches 94; Conservative .15; Mismatches 11; Indels 0; Gaps 0;

OY      1  EVOLOOGSAELVKGASVRLSKKASGYTFNFYIYWKORPGGLEWIGELINPBGDTDF 60
       :|||||
Db      7  qvdlqsgaelvkgasvrlskkasytlftsymhwkqrpgrglewigrldpnsqgltky 66
       :|||||
OY      61 NEKFESRALTVDKSSSTAYMQLSLTSEDSAIYCTRSPYGNNGFTYWGQGLTVTVA 120
       :|||||
Db      67 nekfkakltvdkpsstaymqjssltssedsavycarydygssyfdywgqglvtvts 126

RESULT  4
R22584  R22584 standard; Protein: 256 AA.
XX
AC      R22584;
XX
DT      21-MAY-1992 (first entry)
XX
DE      scfVb18 construct #3.
XX
KM      fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KM      plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KM      specific binding pairs; replicable genetic display package.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 236      /label= mutation
FT      /note=" Ser -> Gly (VL CDR3) "
XX
PN      MO9201047-A.
XX
PD      23-JAN-1992.
XX
PF      10-JUL-1991; 91WO-GB01134.
XX
PR      15-MAY-1991; 91GB-0010549.
PR      10-JUL-1990; 90GB-0015198.
PR      19-OCT-1990; 90GB-0022845.
PR      12-NOV-1990; 90GB-0024503.
PR      06-MAR-1991; 91GB-0004744.
XX
PA      (CAMB-) CAMBRIDGE ANTIBODY.
XX      (MED-) MED RES COUNCIL.
XX
PI      McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI      Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI      Winter GP, Bonnett TP;
XX
DR      WPI: 1992-056862/07.
DR      N-PSDB; Q23860.
XX
PT      Producing members of specific binding pairs - by expression in
PT      recombinant host cells with a secreting replicable genetic
PT      display package.
XX

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PS Example 38; Fig 44; 209pp; English.

XX The sequence is encoded by an antibody scfv fragment directed

CC against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of

CC an MAb against NP were separately amplified and reassembled to form

CC the construct, which was then ligated into the fd gene III contg.

CC vector, fdCAT2, derived from fdtps/Xh. (See Q21095). The clone having

CC the scfvB18 sequence fused in frame to gene III was designated

CC fdCAT2scfvB18. Alternatively the fragment was cloned into fdDogkan

CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)

CC to give fdDogkanscfvB18, or into the phagemid pHEM1 to create pHEM1-

CC scfvB18. The constructs were used to test the effect of using muta-

CC tor strains to increase the diversity of the cloned genes. The

CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046

CC mutT1::Tn10 were constructed by pl transduction. After 4 rounds of

CC mutation and screening, 40 phage inserts were sequenced. They each

CC displayed single mutations in 6 different positions, five being in

CC the light chain region. More than 70% of the mutations occurred at

CC positions 724 and 725 (of the nucleotide sequence) changing the

CC first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp

CC (in 3 cases). The mutant shown here occurred once. The mutant

CC fragments had affinities for NP which were comparable to the wild-

CC type scfv fragment (20nM).

CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.

CC See also R21260-307, 309-311; R22450, 565-581.

XX Sequence 256 AA;

SO

Query Match 80.1%; Score 511; DB 13; Length 256;

Best Local Similarity 78.3%; Pred. No. 1,76-37;

Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

OY 1 EVOLQSGAEIVKPGASVYKLSCKASGYTFYVFWKQRPQGLWIGETINPRNGDTDF 60

Db 7 qvqlqsgaeivkpgasvklscakasygftlsymhwvqrpgrglewlgtrldpnsqgltky 66

OY 61 NEKESRATLVNDRSSSTAYWQLSLTSEDSAIYYCTSPYGNNGYFGTYWQGLTVTVSA 120

Db 67 nekfskaltlvdkpsstaymqsltsedsavycarydygssytdfwgqgtltvss 126

RESULT 5

R22585 ID R22585 standard; Protein: 256 AA.

AC R22585;

XX 21-MAY-1992 (first entry)

DT XX

DE ScfvB18 construct #4.

XX

XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;

KW plus; g3p; binding; adsorption; gene VIII; diverse repertoire;

KM specific binding pairs; replicable genetic display package.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 242

FT /label= mutation

FT /note= Gly -> Ser (VL FR4) "

XX

PN MO9201047-A.

XX

PD 23-JAN-1992.

XX

PF 10-JUL-1991; 91WO-GB01134.

XX

XX 15-MAY-1991; 91GB-0010549.

PR 10-JUL-1990; 90GB-0015198.

PR 19-OCT-1990; 90GB-0022845.

PR 12-NOV-1990; 90GB-0024503.

PR 06-MAR-1991; 91GB-0004744.

XX

XX (CAMB-) CAMBRIDGE ANTIBODY.

PA (MEDT-) MED RES COUNCIL.

XX

XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRU, Griffiths AD;

PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;

PI Walter GP, Bonnett TP;

XX

DR WPL: 1992-056862/07.

DR N-PSDB: Q23861.

XX

PT Producing members of specific binding pairs - by expression in

PT recombinant host cells with a secreting replicable genetic

PT display package.

XX

PS Example 38; Fig 44; 209pp; English.

XX

XX The sequence is encoded by an antibody scfv fragment directed

CC against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of

CC an MAb against NP were separately amplified and reassembled to form

CC the construct, which was then ligated into the fd gene III contg.

CC vector, fdCAT2, derived from fdtps/Xh. (See Q21095). The clone having

CC the scfvB18 sequence fused in frame to gene III was designated

CC fdCAT2scfvB18. Alternatively the fragment was cloned into fdDogkan

CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)

CC to give fdDogkanscfvB18, or into the phagemid pHEM1 to create pHEM1-

CC scfvB18. The constructs were used to test the effect of using muta-

CC tor strains to increase the diversity of the cloned genes. The

CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046

CC mutT1::Tn10 were constructed by pl transduction. After 4 rounds of

CC mutation and screening, 40 phage inserts were sequenced. They each

CC displayed single mutations in 6 different positions, five being in

CC the light chain region. More than 70% of the mutations occurred at

CC positions 724 and 725 (of the nucleotide sequence) changing the

CC first Gly in the J segment (framework 4) to Ser (in 21 cases), as

CC shown here) or Asp (in 3 cases). The mutant fragments had affin-

CC ties for NP which were comparable to the wild-type scfv fragment

CC (20nM).

CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.

CC See also R21260-307, 309-311; R22450, 565-581.

XX

XX Sequence 256 AA;

SO

Query Match 80.1%; Score 511; DB 13; Length 256;

Best Local Similarity 78.3%; Pred. No. 1,76-37;

Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

OY 1 EVOLQSGAEIVKPGASVYKLSCKASGYTFYVFWKQRPQGLWIGETINPRNGDTDF 60

Db 7 qvqlqsgaeivkpgasvklscakasygftlsymhwvqrpgrglewlgtrldpnsqgltky 66

OY 61 NEKESRATLVNDRSSSTAYWQLSLTSEDSAIYYCTSPYGNNGYFGTYWQGLTVTVSA 120

Db 67 nekfskaltlvdkpsstaymqsltsedsavycarydygssytdfwgqgtltvss 126

RESULT 6

R22586 ID R22586 standard; Protein: 256 AA.

AC R22586;

XX 21-MAY-1992 (first entry)

DT XX

DE ScfvB18 construct #5.

XX

XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;

KW plus; g3p; binding; adsorption; gene VIII; diverse repertoire;

KM specific binding pairs; replicable genetic display package.

XX

OS Synthetic.



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XX Key Location/Qualifiers
FH MISC-difference 242 /label= mutation
FT /note=" Gly -> Asp (VL FR4) "
XX
XX WO9201047-A.
XX
XX 23-JAN-1992.
XX
XX 10-JUL-1991: 91WO-GB01134.
XX
XX 15-MAY-1991: 91GB-0010549.
XX 10-JUL-1990: 90GB-0015198.
XX 19-OCT-1990: 90GB-0022845.
XX 12-NOV-1990: 90GB-0024503.
XX 06-MAR-1991: 91GB-0004744.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY.
XX (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
XX Winter GP, Bonnett TP;
XX
XX WPI: 1992-056662/07.
XX N-PSDB: Q23862.
XX
XX Producing members of specific binding pairs - by expression in
XX recombinant host cells with a secreting replicable genetic
XX display package.
XX
XX Example 38; Fig 44; 209pp; English.
XX
XX The sequence is encoded by an antibody scfv fragment directed
XX against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
XX an MAb against NP were separately amplified and reassembled to form
XX the construct, which was then ligated into the fd gene III contg.
XX vector, fdCAT2, derived from fdgfp/Xh. (See Q21095). The clone having
XX the scfVB18 sequence fused in frame to gene III was designated
XX fdCAT2scfVB18. Alternatively the fragment was cloned into fdDOGkan
XX (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
XX to give fdDOGkanscfVB18, or into the phagemid pHEM1 to create pHEM1-
XX scfVB18. The constructs were used to test the effect of using muta-
XX tor strains to increase the diversity of the cloned genes. The
XX strains NR9046mutD5::Tn10 and NR9046mutT1: NR9046
XX mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
XX mutation and screening, 40 phage inserts were sequenced. They each
XX displayed single mutations in 6 different positions, five being in
XX the light chain region. More than 70% of the mutations occurred at
XX positions 724 and 725 (of the nucleotide sequence) changing the
XX first gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
XX (in 3 cases, as shown here). The mutant fragments had affinities
XX for NP which were comparable to the wild-type scfv fragment (20nM).
XX N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
XX See also R21260-307, 309-311; R22450, 565-581.
XX
XX Sequence 256 AA:
XX
XX Query Match 80.1%; Score 511; DB 13; Length 256;
XX Best Local Similarity 78.3%; Pred. No. 1,7e-37;
XX Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;
XX
XX 1 EVQLOOSGAEIVKPGASVYLSGASGYTFTNFIYVWKRPGGLEWIGEINPRNDTDP 60
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 7 gqyldqsgaeivkpgasvylscasgytftsywmhvkrpgrglewigrldpnsqgltly 66
XX
XX 61 NEKFESRALITVDRKSSSTYMOGLSLTSEDATYCTRRSPYGNNGYFTYMOGQTLTVTSA 120
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 67 nekfkakeltvdkspsstymqsltsedsavyyrcarydygssyfdywgqgtltvss 126
XX

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RESULT 7
R22587
ID R22587 standard; Protein: 256 AA.
XX
XX R22587;
XX
XX 21-MAY-1992 (first entry)
XX
XX ScfVB18 construct #6.
XX
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
XX plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH MISC-difference 245 /label= mutation
FT /note=" Thr -> Ile (VL FR4) "
XX
XX WO9201047-A.
XX
XX 23-JAN-1992.
XX
XX 10-JUL-1991: 91WO-GB01134.
XX
XX 15-MAY-1991: 91GB-0010549.
XX 10-JUL-1990: 90GB-0015198.
XX 19-OCT-1990: 90GB-0022845.
XX 12-NOV-1990: 90GB-0024503.
XX 06-MAR-1991: 91GB-0004744.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY.
XX (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
XX Winter GP, Bonnett TP;
XX
XX WPI: 1992-056662/07.
XX N-PSDB: Q23863.
XX
XX Producing members of specific binding pairs - by expression in
XX recombinant host cells with a secreting replicable genetic
XX display package.
XX
XX Example 38; Fig 44; 209pp; English.
XX
XX The sequence is encoded by an antibody scfv fragment directed
XX against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
XX an MAb against NP were separately amplified and reassembled to form
XX the construct, which was then ligated into the fd gene III contg.
XX vector, fdCAT2, derived from fdgfp/Xh. (See Q21095). The clone having
XX the scfVB18 sequence fused in frame to gene III was designated
XX fdCAT2scfVB18. Alternatively the fragment was cloned into fdDOGkan
XX (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
XX to give fdDOGkanscfVB18, or into the phagemid pHEM1 to create pHEM1-
XX scfVB18. The constructs were used to test the effect of using muta-
XX tor strains to increase the diversity of the cloned genes. The
XX strains NR9046mutD5::NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
XX mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
XX mutation and screening, 40 phage inserts were sequenced. They each
XX displayed single mutations in 6 different positions, five being in
XX the light chain region. More than 70% of the mutations occurred at
XX positions 724 and 725 (of the nucleotide sequence) changing the
XX first gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
XX (in 3 cases). The mutant shown here occurred once. The mutant
XX fragments had affinities for NP which were comparable to the wild-
XX type scfv fragment (20nM).
XX N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
XX See also R21260-307, 309-311; R22450, 565-586.
XX

```

Seq	Sequence	256 AA:
00	Query Match	80.1%; Score 511; DB 13; Length 256;
00	Best Local Similarity	78.3%; Pred. NO. 1.7e-37;
00	Matches	94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;
01	1	EVOLDOOSGAELVKPCASVYKLSCKASGYFTTNFEIYWKORPOGGLWEIGINPRNGDTDF 60
02	7	qyqlqsgsaelvkvpsavkylsckaagylftsywmhwkqrpgrglewlgripnsggkly 66
03	61	NEKFSRATLVNDKSSSTAYWOLSLTSDSAIYCTRSPPGNNGFTYYGGCTLVTVSA 120
04	67	nekfkskatltvdkpsstaysltsedsavyyccarydygssyfydygsgtltvss 126
05	RESULT 8	
06	R79863	
07	ID	R79863 standard; Protein; 119 AA.
08	AC	R79863;
09	XX	
10	DT	02-JUL-1996 (first entry)
11	XX	
12	DE	Anti-EGFR antibody heavy chain variable region (Clone L3 11D).
13	XX	
14	KM	Single chain antibody; antibody; epidermal growth factor receptor;
15	KW	EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
16	KM	assessment; phage antibody library.
17	XX	
18	OS	Mus musculus.
19	XX	
20	PN	WO9525167-A1.
21	PD	21-SEP-1995.
22	XX	
23	PF	16-MAR-1995; 95WO-EP00978.
24	XX	
25	PR	02-DEC-1994; 94EP-0118970.
26	XX	17-MAR-1994; 94EP-0104160.
27	XX	
28	PA	(MERE) MERCK PATENT GMBH.
29	XX	
30	PI	Aden J, Ansell KH, Bendig MM, Blasco F, Guessow D;
31	PI	Kettleborough AC, Miltjans F, Pluats J, Rosell E;
32	DR	WPI; 1995-336972/43.
33	DR	N-PSDB; T04016.
34	XX	
35	PT	Anti-EGFR antibodies and single chain Fv antibody fragments -
36	PT	obtained from phage-antibody libraries, useful for diagnosis and
37	PT	therapy of tumours
38	XX	
39	PS	Claim 4; Page 53; 93pp; English.
40	XX	
41	CC	Anti-epidermal growth factor receptor (EGFR) single chain antibodies
42	CC	and antibodies constructed from anti-EGFR antibody fragments can be
43	CC	used for diagnosis of tumours and assessment of tumour growth in
44	CC	vitro and in vivo. They may also be used in a pharmaceutical
45	CC	composition for the therapy of e.g. melanomas, gliomas and carcinomas.
46	CC	The antibodies and fragments are derived from mice but are humanised
47	CC	so as to cause minimum reaction against them. They are produced
48	CC	using the phage antibody library. (See T04011-T04026 and
49	CC	R79858-R79873)
50	XX	
51	Sequence	119 AA;
52	Query Match	79.5%; Score 507.5; DB 16; Length 119;
53	Best Local Similarity	79.2%; Pred. NO. 1.6e-37;
54	Matches	95; Conservative 16; Mismatches 8; Indels 1; Gaps 1;
55	1	EVOLDOOSGAELVKPCASVYKLSCKASGYFTTNFEIYWKORPOGGLWEIGINPRNGDTDF 60

Db	1	evqlqgsgaaevkpgasvklscasgytlfsgymhvkqirpqlgawlgeldpslsy	60
Oy	61	NEKESRATLTVDKSSSTAYWQULSSTEDSAIYCTRSRPNNGYFTYWGCTLVTVSA	120
Db	61	ngkftgkattlvdkssstaymqsltsedsavyycaisdgyssh-fdywsgtltvss	119
RESULT	9		
W04332			
ID	W04332	standard; peptide; 119 AA.	
AC	W04332;		
DT	23-JUN-1997	(first entry)	
DE	Heavy chain of monoclonal antibody 4B4-1-1.		
KM	Antibody: human; heavy chain; variable region; light chain; MAb; 4-1B;		
KM	Tumour necrosis factor receptor; membrane protein; accessory molecule;		
KM	T-cell; antigen-presenting cell; immune response; rheumatoid arthritis;		
KM	immunosuppressive agent; autoimmune disease; rejection response; therapy;		
KM	organ transplantation.		
OS	Synthetic.		
Key	Location/Qualifiers		
FT	Region	31..35	
FT	/note=	"complementarity determining region 1"	
FT	Region	50..66	
FT	/note=	"complementarity determining region 2"	
FT	Region	99..108	
FT	/note=	"complementarity determining region 3"	
PM	W09632495-A1.		
PD	17-OCT-1996.		
PE	06-APR-1996;	96WO-KR00045.	
PR	08-APR-1995;	95KR-0008176.	
PA	(GLDS ) LG CHEM LTD.		
PI	Kang CY, Kim JG;		
PI	WPI: 1996-477145/47.		
DR	N-PSDB; T38509.		
PT	Monoclonal antibody specific for human 4-1BB - useful as		
PT	immunospecific agent for treating autoimmune diseases and preventing		
PT	organ transplant rejection		
PS	Claim 2; Page 23; 37pp: English.		
XX	W04332 and W04333 represent fragments of the variable regions of the		
CC	heavy and light chains of the antibody of the invention. This sequence is		
CC	encoded by nucleotides 109 to 465 of the coding sequence shown in T38509.		
CC	The antibody of the invention (designated 4B4-1-1) is a monoclonal		
CC	antibody (Mab) specific for human 4-1BB. 4-1BB encodes a member of the		
CC	tumour necrosis factor receptor family of integral membrane proteins.		
CC	4-1BB is an accessory molecule expressed on the surface of T-cells in the		
CC	initial stage of activation. The accessory molecules on the T-cell bind		
CC	to the corresponding ligand on the antigen-presenting cell and this		
CC	accelerates the activation of the T- and antigen-presenting cells,		
CC	thereby promoting various immune responses. The Mab is specific for human		
CC	4-1BB, which is selectively expressed on activated T-cells. The Mab is		
CC	useful as an immunosuppressive agent. It can be used for the treatment of		
CC	autoimmune diseases, such as rheumatoid arthritis, and for preventing		
CC	rejection response after organ transplantation.		
SC	Sequence	119 AA;	

```

Query Match Similarity      79.4%; Score 506.5; DB 17; Length 119;
Best Local Similarity      80.8%; Pred. No. 1.9e-37;
Matches 97; Conservative 12; Mismatches 10; Indels 1; Gaps 1
OY 1 EVOLQOOSGAELVKKPASVYKLSCKASGYFTNFYIYVWKORPCQGLEWIEINPRNDTDF 60
Db 1 qvqlqgpaelvkkpasvylksckasgyfttsywmhmwvkqrpqglvlelginpghntly 60
OY 61 NEKFSRATLTVDKSSSTAYMOLSLTSDSAIYYCTRSPPYGNNG--FTYWGQGLTVTV 120
Db 61 nekfskatltvdkssstaymqsltsedsavyycars-ftlgrfayvggqlvtvsa 119

RESULT 10
R84555
ID R84555 standard; Protein; 122 AA.
XX
XX R84555;
XX
XX 02-FEB-1996 (first entry)
XX
XX B-cell lymphoma CH12 Igm heavy chain.
XX DE
XX Monoclonal antibody; Mab; SCH94.03; hybridoma; central nervous system;
XX CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
XX B-cell lymphoma; CH12; Igm.
XX
XX Mus sp.
XX OS
XX MO9530004-A1.
XX PN
XX 09-NOV-1995.
XX PD
XX 27-APR-1995; 95MO-US05262.
XX PE
XX 29-APR-1994; 94US-0236520.
XX PR
XX (MAYO-) MAYO FOUNDATION.
XX PA
XX Miller DJ, Rodriguez M.
XX PI
XX WPI; 1995-393077/50.
XX DR
XX N-PSDB; T05314.
XX DR
XX
XX Monoclonal antibodies which stimulate central nervous system
XX PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
XX PT treating multiple sclerosis, and viral or post-neural diseases of
XX PT the CNS.
XX
XX Disclosure; Page 40; 63pp; English.
XX PS
XX
XX The heavy chain variable region amino acid sequence (given
XX CC in R84554) of monoclonal antibody SCH94.03 shows extensive sequence
XX CC similarity with the corresp. sequence (R84555) of the Igm produced
XX CC by B-cell lymphoma CH12.
XX CC
XX
XX Sequence 122 AA;
XX SO

Query Match      78.5%; Score 501; DB 16; Length 122;
Best Local Similarity 77.0%; Pred. No. 5.9e-37;
Matches 94; Conservative 15; Mismatches 11; Indels 2; Gaps 1
OY 1 EVOLQOOSGAELVKKPASVYKLSCKASGYFTNFYIYVWKORPCQGLEWIEINPRNDTDF 60
Db 1 qvqlqgpaelvkkpasvylksckasgyfttsywmhmwvkqrpqglvlelginpghntly 60
OY 61 NEKFSRATLTVDKSSSTAYMOLSLTSDSAIYYCTRSPPYGNNG--FTYWGQGLTVTV 118
Db 61 nekfskatltvdkssstaymqsltsedsavyyrardiygsswgyyldyvggqflltly 120
OY 119 SA 120

```

Db		: ss 122
RESULT	11	
ID	V71473	standard; Protein; 119 AA.
XX	AC	Y71473;
XX	DF	04-OCT-2000 (first entry)
XX		
XX		Mouse monoclonal antibody 4B4-1-1, heavy chain variable region (VH).
DE		
KW		Humanised antibody; H24B4h-1; human 4-1BB receptor protein; mouse;
KW		light chain variable region; VL; heavy chain variable region; VH; Mab;
KW		monoclonal antibody; 4B4-1-1; complementarity determining region; CDR;
KW		FR; framework region; treat; transplant rejection; rheumatoid arthritis;
KW		autoimmune disease; immunosuppressant; antirheumatic; antiarthritic.
XX		
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	Region	31..35
FT		/label= CDR 1
FT		/note= "Complementarity determining region"
FT	Region	50..66
FT		/label= CDR 2
FT		/note= "Complementarity determining region"
FT	Region	99..108
FT		/label= CDR 3
FT		/note= "Complementarity determining region"
PN		WO200029445-A1.
PD	25-MAY-2000.	
XX		
PF	17-NOV-1999;	99WO-KR00689.
XX		
PR	17-NOV-1998;	98KR-0049177.
PR	11-MAY-1999;	99KR-0016750.
XX		
PA	(GLDS ) LG CHEM LTD.	
PI	Hong HJ, Park SS, Kang YJ, Kang CY, Yoon SK;	
XX		
DR	WI: 2000-387750/33.	
DR	N-PSDB; D01263.	
PT		Humanized antibody specific for human 4-1BB, the composition comprising
PT		the antibody useful for treating autoimmune diseases e.g. rheumatoid
PT		arthritis or as an immuno suppressant to prevent graft rejection -
XX		
PS	Example 1; Fig 2; 83pp; English.	
XX		
CC		The present amino acid sequence is the mouse monoclonal antibody
CC		(Mab) 4B4-1-1, heavy chain variable region (VH). The complementarity
CC		determining region (CDR) of this sequence is used to construct the
CC		humanised antibody H24B4h-1, heavy chain variable region, specific
CC		to the human 4-1BB protein receptor. In order to increase the antigen
CC		binding affinity of the humanised antibody H24B4h-1, critical amino acid
CC		substitutions are made in the framework region (FR) of the humanised VH,
CC		to resemble the mouse antibody. H24B4h-1 functions to block human 4-1BB
CC		protein receptor. The humanised antibody can be used to treat autoimmune
CC		diseases, especially rheumatoid arthritis and for immune suppression in
CC		transplant rejection. It acts as an effective immunosuppressant, by
CC		inhibiting T cell activation, without any adverse side effects.
XX		
SQ	Sequence	119 AA;

Query Match 78.4%; Score 500.5; DB 21; Length 119;  
 Best Local Similarity 80.0%; Pred No. 6,4e-37;

Matches	96:	Conservative	12:	Mismatches	11:	Indels	1:	Gaps	1:
Oy	1	EVOLDOOGSAELVYKPGASVYKLSCKASGYFTTNYFIYWKORPGOGLEWIGEINPRNGDTE	60	1	EVOLDOOGSAELVYKPGASVYKLSCKASGYFTTNYFIYWKORPGOGLEWIGEINPRNGDTE	60			
Db	1	qyqlqgpaqaelvkvpaasvklscakasytfsyywmhvkqpgqvlawigelnpgnhtny	60	1	qyqlqgpaqaelvkvpaasvklscakasytfsyywmhvkqpgqvlawigelnpgnhtny	60			
Oy	61	NEKFESRATLVYDKSSSTAYVMQLSITSDSAIYYCTRSPYGNNGFTYWGQGLVTVSA	120	61	NEKFESRATLVYDKSSSTAYVMQLSITSDSAIYYCTRSPYGNNGFTYWGQGLVTVSA	120			
Db	61	nekfkskatlvckssstaymqjssltssedssavyycaars-ftlara fayqgqglv tvsa	119	61	nekfkskatlvckssstaymqjssltssedssavyycaars-ftlara fayqgqglv tvsa	119			
RESULT	12								
ID	W02291	W02291 standard; Protein; 139 AA.							
XX	AC	W02291:							
XX	DT	22-NOV-1996 (first entry)							
XX	DE	FVKC-II VH region.							
XX	KW	Single chain antibody; Fv; FVKC; heavy chain; light chain;							
KW	antibody engineering; peptide hormone; pichia pastoris.								
XX	OS	Mus musculus.							
XX	Key	Location/Qualifiers							
FT	Peptide	1..22							
FT	Protein	/label= PeIB_leader							
FT		23..139							
XX		/label= VHKC							
PN	W0962/612-A1.								
XX	12-SEP-1996.								
XX	PD								
PE	01-MAR-1996;	96WO-GB00468.							
XX	03-MAR-1995;	95GB-0004344.							
XX	(UNIL ) QUEST INT BV.								
PI	Berry MJ, Davis PJ, Van Der Logt CPE, Whitelam GC;								
XX	WPI; 1996-425380/42.								
DR	N-PSDB; T36906.								
PT	Prodn. of antibody fragments, partic. in yeast - by prodn. of heavy								
PT	and light chains linked by sequence cleavable by host enzyme								
XX	Disclosure: Fig 8; 53pp; English.								
XX	FVKC VH (W02291) and VL (W02292) chains are encoded by a DNA								
CC	construct (T36906) assembled in E. coli vector pUC19. FVKC								
CC	is a single-chain antibody that shows specificity for a peptide								
CC	hormone. Novel antibody fragments (see also W02293-94) have								
CC	been constructed in which the FVKC VH and VL chains are separated								
CC	by a KEX2-type processing sites, allowing prodn. in yeast, partic.								
CC	Pichia pastoris, host cells.								
XX									
SO	Sequence 139 AA:								
Query Match	78.4%; Score 500.5; DB 17; Length 139;								
Best Local Similarity	80.8%; Pred. No. 7.5e-37;								
Matches	97: Conservative 11; Mismatches 9; Indels 3; Gaps 2								
Oy	1	EVOLDOOGSAELVYKPGASVYKLSCKASGYFTTNYFIYWKORPGOGLEWIGEINPRNGDTE	60						
Db	23	qyqlqgpaqaelvkvpaasvklscakasytfsyywmhvkqpgqvlawigelnpgnhtny	82						
Oy	61	NEKFESRATLVYDKSSSTAYVMQLSITSDSAIYYCTRSPYGNNGFTYWGQGLVTVSA	120						
Db	61	nekfkskatlvckssstaymqjssltssedssavyycaars-ftlara fayqgqglv tvsa	119						

```
Db      63 nekfkskellvdkssstslaymlssltsedsavvyarr-ygns--fdywgqglvtvrs 139
RESULT 13
ID      W02294
AC      W02294 standard; Protein; 252 AA.
XX
XX      W02294;
XX
XX      22-NOV-1996 (first entry)
XX
XX      Yeast-FVKC-II-KEX2.
DE
KW      Single chain antibody; Fv; FVKC; heavy chain; light chain;
KM      antibody engineering; peptide hormone; pichia pastoris; KEX2.
XX
XX      Chimeric Mus musculus;
OS      Chimeric synthetic.
XX
FH      Key Location/Qualifiers
FT      Domain 1...120
FT      /label= VHRC
FT      Cleavage-site 121..125
FT      /note= "KEX2 cleavage site"
FT      Domain 126..239
FT      /label= VLKC
FT      Peptide 240..252
FT      /label= Hydrophil-II-tag
FT      /note= "facilitates Fv assay"
XX
XX      WO9627612-A1.
XX
XX      12-SEP-1996.
XX
XX      01-MAR-1996; 96WO-GB00468.
XX
XX      03-MAR-1995; 95GB-0004344.
XX
XX      (UNIL ) QUEST INT BV.
PA
PI      Berry MJ, Davis PJ, Van Der Logt CPE, Whitelam GC;
XX
XX      WPI: 1996-425380/42.
DR      N-PsDB: T36908.
DR      P-PsDB: W02292.
XX
XX      Prodn. of antibody fragments, partic. in yeast - by prodn. of heavy
PT      and light chains linked by sequence cleavable by host enzyme
XX
XX      Disclosure: fig 10; 53pp; English.
PS
XX      Yeast-FVKC-II-KEX2 (W02294) comprises a KEX2-type processing site
CC      positioned between the VH and VL chains of peptide hormone-specific
CC      FvHK (see also W02291-92). DNA (T36908) coding for
CC      yeast-FVKC-II-KEX2 can be incorporated into vector pPIC9 for prodn.
CC      of FVKC-II-KEX2 in pichia pastoris. This illustrates a process for
CC      prodn. of antibody fragments in which the VH and LH regions are
CC      linked by a sequence cleavable by a host enzyme. The VH and VL are
CC      produced by the yeast in equal amounts as separate chains which are
CC      free to associate and fold.
XX
SQ      Sequence 252 AA:

Query Match          78.4%; Score 500.5; DB 17; Length 252;
Best Local Similarity 80.8%; Pred. No. 1,4e-36;
Matches 97; Conservative 11; Mismatches 9; Indels 3; Gaps 2.;
```

Db 64 nekfskaltlvdkssstaymqjssltssdsavyycaarr-ygns--fdywgqglvtvss 120

## RESULT 14

W02293 standard; Protein; 271 AA.

AC W02293;

DT 22-NOV-1996 (first entry)

DE FVHC-II-KEX2.

KM Single chain antibody; Fv; FVHC; heavy chain; light chain;  
KW antibody engineering; peptide hormone; Pichia pastoris; KEX2.

OS Chimeric Mus musculus;  
XX Chimeric synthetic.

FT Key Location/Qualifiers

FT Peptide 1..22 /label= pelb\_leader

FT Domain 23..139 /label= VHHC

FT Cleavage-site 140..144 /note= "KEX2 cleavage site"

FT Domain 144..258 /label= VLKC

FT Peptide 259..271 /label= "Hydrophil-IL tag  
/note= "facilitates Fv assay"

PN W09627612-A1.

PD 12-SEP-1996.

PF 01-MAR-1996; 96WO-GB00468.

PR 03-MAR-1995; 95GB-0004344.

XX (UNIL ) QUEST INT BV.

PA Berry MJ, Davis PJ, Van Der Logt CPE, Whitelem GC;

PI WPI, 1996-425380/42.

DR N-PSDB; T36907.

DR P-PSDB; W02292.

XX Prod. of antibody fragments, partic. in yeast - by prodn. of heavy  
PT and light chains linked by sequence cleavable by host enzyme

XX Disclosure; Fig 9; 53pp; English.

CC FVHC-II-KEX2 (W02293) comprises a KEX2-type processing site  
CC positioned between the VH and VL chains of peptide hormone-specific

CC FvKH. DNA (T36907) coding for FvHC-II-KEX2 can be incorporated  
CC into vector pPIC9 (see also T36908) for prodn. of FVHC-II-KEX2 in

CC Pichia pastoris. This illustrates a process for prodn. of  
CC antibody fragments in which the VH and LH regions are linked  
CC by a sequence cleavable by a host enzyme.

XX Sequence 271 AA;

Query Match 78.4%; Score 500.5; DB 17; Length 271;

Best local Similarity 80.8%; Pred. No. 1.5e-36; Mismatches 9; Indels 3; Gaps 2;

QY 1 EVOLQSGALVLPAGASVKSCKASGYTFTNYFIYWKQRPQGLWIGELINPNDGDTDF 60  
DB 23 qvqlqgsaelvlpagsvksckasgytfttsymhvwkfpqgslwlgelinpndgrtyy 82

QY 61 NEKFSRATLVTDKSSSTAYMQLSLTSEDSALYYCTRSPYGNNGFTYWGQGLTVTVA 120  
DB 83 nekfskaltlvdkssstaymqjssltssdsavyycaarr-ygns--fdywgqglvtvss 139

## RESULT 15

P70624 standard; Protein; 136 AA.

AC P70624;

DT 09-APR-1991 (first entry)

DE Sequence encoded by anti-hepatitis B heavy chain variable region in  
DE PING2006E.

KM Chimeric antibody; Anti-cancer antibody.

PN W08702671-A.

PD 07-MAY-1987.

PF 27-OCT-1986; 86WO-US02269.

PR 01-NOV-1985; 85US-0793980.

PA (ITGE-) INT GENETIC ENG INC.  
(ROBI/) ROBINSON R R.

PI Robinson RR, Liu AY, Horwitz AH, Wall R;

DR WPI: 1987-136004/19.

DR N-PSDB; N70967, N70968.

XX Prod. of immunoglobulin chains and molecules - is by recombinant  
PT DNA procedures, with chimeric antibodies etc. related to cancer  
PT specific antigens.

XX Example; Fig 12B; 126pp; English.

CC The patentors claim a chimeric antibody molecule comprising 2 light  
CC chains and 2 heavy chains, each comprising a constant human region  
CC and a variable non-human region. Coding sequences for the Ig chains  
CC are also claimed. The invention provides consensus sequences of

CC light and heavy chain J regions useful in the design of  
CC oligonucleotides (UIGs) for use as primers or probes for cloning

CC immunoglobulinlight or heavy chain mRNAs or genes. Depending on the  
CC nature of design of a particular URG, it may be capable of

CC hybridizing to all Ig mRNAs or genes containing a single specific J  
CC sequence. UIG denotes universal immunoglobulin gene.

XX Sequence 136 AA;

Query Match 78.0%; Score 497.5; DB 8; Length 136;

Best local Similarity 78.3%; Pred. No. 1.3e-36; Mismatches 10; Indels 3; Gaps 1;

QY 1 EVOLQSGALVLPAGASVKSCKASGYTFTNYFIYWKQRPQGLWIGELINPNDGDTDF 60  
DB 20 qvqlqgsaelvlpagsvksckasgytfttsymhvwkfpqgslwlgelinpndgrtyy 79

QY 61 NEKFSRATLVTDKSSSTAYMQLSLTSEDSALYYCTRSPYGNNGFTYWGQGLTVTVA 120  
DB 80 nekfskaltlvdkssstaymqjssltssdsavyycaasydyd--wfaywgqglvtvss 136

Search completed: June 20, 2001, 11:15:22  
Job time: 1663 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: June 20, 2001, 11:18:20 ; Search time 107.93 Seconds

(without alignments)  
134.843 Million cell updates/sec

Title: US-09-615-872-2

Sequence: 1 AEDDIQMISQKFMSTSVGD.....COQYNSYPLRTGTGKLEIK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
SPREMBL_16:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.unclassified:*
13: sp.vertebrate:*
14: sp.virus:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	67.1	108	4 Q9UL70	Q9UL70 homo sapien
2	383	66.6	99	11 Q9UL74	Q9UL74 mus musculu
3	367	63.8	108	4 Q9UL79	Q9UL79 homo sapien
4	364	63.3	108	4 Q9UL77	Q9UL77 homo sapien
5	356.5	62.0	109	4 Q9UL85	Q9UL85 homo sapien
6	356	61.9	108	4 Q9UL83	Q9UL83 homo sapien
7	355.5	61.8	107	4 Q9UL81	Q9UL81 homo sapien
8	348.5	60.6	109	4 Q9UL78	Q9UL78 homo sapien
9	344	59.8	107	11 Q9ER29	Q9ER29 mus musculu
10	342	59.5	114	11 Q9RIAS	Q9RIAS mus musculu
11	333	56.2	107	11 Q9UL84	Q9UL84 mus musculu
12	315.5	54.9	109	4 Q9UL86	Q9UL86 mus musculu
13	313.5	54.5	106	5 Q9UL10	Q9UL10 schistosoma
14	310	53.9	298	11 Q9GYFO	Q9GYFO mus musculu
15	308.5	53.7	104	11 Q9UL82	Q9UL82 mus musculu
16	296	51.5	103	11 Q9UL80	Q9UL80 mus musculu
17	287	49.9	97	11 Q9UL76	Q9UL76 mus musculu
18	287	49.9	101	11 Q9UL78	Q9UL78 mus musculu
19	276	48.0	114	4 Q9UL80	Q9UL80 homo sapien

20	254	44.2	109	6 Q9NDM5	Q9NDM5 cryotolagus
21	227	39.5	107	4 Q9NSD6	Q9NSD6 homo sapien
22	205.5	35.7	107	4 Q9UL82	Q9UL82 homo sapien
23	179	31.1	109	11 Q9ET13	Q9ET13 mus musculu
24	159	27.7	130	4 Q9NP29	Q9NP29 homo sapien
25	137.5	23.9	334	13 Q9IB05	Q9IB05 spherooides
26	134	23.3	135	4 Q9H524	Q9H524 homo sapien
27	132.5	23.0	93	4 Q9UL76	Q9UL76 homo sapien
28	130.5	22.7	123	11 Q61243	Q61243 mus musculu
29	130.5	22.7	337	13 Q9IB02	Q9IB02 spherooides
30	122	21.2	235	4 Q9H101	Q9H101 homo sapien
31	119	20.7	320	13 Q9IA29	Q9IA29 spherooides
32	110.5	19.2	337	13 Q9IA24	Q9IA24 spherooides
33	107	18.6	372	4 Q9Y4V0	Q9Y4V0 homo sapien
34	106.5	18.5	122	4 Q99604	Q99604 homo sapien
35	106	18.4	361	4 Q9H1U5	Q9H1U5 homo sapien
36	105.5	18.3	122	4 Q99603	Q99603 homo sapien
37	105.5	18.3	137	4 Q9UDR1	Q9UDR1 homo sapien
38	105	18.3	342	13 Q9IB00	Q9IB00 spherooides
39	103.5	18.0	503	4 P78324	P78324 homo sapien
40	103.5	18.0	509	11 Q08907	Q08907 mus musculu
41	103	17.9	168	4 Q9UQ56	Q9UQ56 homo sapien
42	102.5	17.8	509	11 Q9QX57	Q9QX57 mus musculu
43	102.5	17.8	513	11 P97797	P97797 mus musculu
44	102	17.7	398	4 Q00241	Q00241 homo sapien
45	100.5	17.5	333	13 Q9IB04	Q9IB04 spherooides

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	108 AA.
Q9UL70	Q9UL70			
AC	Q9UL70:			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9827139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Werf P.L., Kallis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
CC	-I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL: AF035044; AAD56280.1; -			
DR	HSSP: P01607; 1RET			
DR	InterPro: IPR003006; -			
DR	InterPro: IPR003596; -			
DR	Pfam: PF00047; 1g; 1.			
DR	SMART: SM00406; 1g; 1.			
FT	NON_TER 1			
FT	NON_TER 108			
SQ	SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;			
Query Match				
Best local similarity 67.1%; Score 386; DB 4; Length 108;				
Matches 72; Conservative 15; Mismatches 20; Indels 0; Gaps 0;				
QY	4 D1QMISQKFMSTSVGDRTVTVCASQNGFTNVAWQQRFGSPNALITSASRYSGVDP 63			
Db	1 D1QMISQKFMSTSVGDRTVTVCASQNGFTNVAWQQRFGSPNALITSASRYSGVDP 60			
QY	64 RFGSGSGTDFLTITNVQSEDLADYFCQYNSYPLRTGTGKLEIK 110			







RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.  
CC EMBL: AF035036; AAD56272.1; -.  
DR HSSP: P01789; IMCP.  
DR Interpro: IPR003006; -.  
DR Interpro: IPR003596; -.  
DR Pfam: PF00047; 1g. 1.  
DR SMART: SM00406; 1g; 1.  
FT NON\_TER 1  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52E2CE197 CRC64;

Query Match 60.6%; Score 348.5; DB 4; Length 109;  
Best Local Similarity 61.1%; Pred. No. 3.2e-30;  
Matches 66; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

QY 4 DIOMIOSQKFMSTVGDVVTYTCASQNVGTN-VAMVQOKPGQSPNALIYSASYRSGVP 62  
DB 1 EIVLTQSPGRTISLSPGERATISCRASQSVSSYLAWYQOKPGQAPRLIYASRRATGIP 60  
63 DRFTGSGSGTDFTLITNVQSEDLADYFCQOQNSYPLFTGTGKLEIK 110  
61 DRFGSGSGTDFTLITSLRLEPDCAVYCOQYSSPLFTFGGTVEIK 108

RESULT 9  
Q9ER29 PRELIMINARY; PRT; 107 AA.

AC Q9ER29;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;  
RT "Cloning and sequencing of the light chain fragment of variable region genes of an anti-tbNF-a monoclonal antibody."  
RL J. Cell. Mol. Immunol. 12:21-26(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RT "Construction and sequencing of the single-chain antibody gene of a human TNF-alpha specific monoclonal antibody."  
RL T1 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF262753; AAC23804.1; -.  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA604A26C3 CRC64;

Query Match 59.8%; Score 344; DB 11; Length 107;  
Best Local Similarity 63.6%; Pred. No. 9.5e-30;  
Matches 66; Conservative 16; Mismatches 17; Indels 6; Gaps 2;

QY 7 MIOGQKFMSTVGDVVTYTCASQNV-GTN-----VAMVQOKPGQSPNALIYSASYRSG 60  
DB 1 MIOGSSLSAVGQKVTMSCKSSQSVLNSNTOKNYLAWYKKPGQSPPELLVYFASTRSG 60  
61 VPDRTGSGSGTDFTLITNVQSEDLADYFCQOQNSYPLFTGTGKTL 107  
|||||

DB 61 VPDRTGSGSGTDFTLITNVQSEDLADYFCQOQHYRTPFTFGSGTKL 107

RESULT 10  
Q9RIAS PRELIMINARY; PRT; 214 AA.

AC Q9RIAS;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramodoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv)."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF152371; AAD40242.1; -.  
DR HSSP: P01789; IMCP.  
DR Interpro: IPR003006; -.  
DR Interpro: IPR003600; -.  
DR Pfam: PF00047; 1g; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
DR SMART: SM00410; IG\_Like; 1.  
FT NON\_TER 1  
FT NON\_TER 214 214  
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDEB995E2A CRC64;

Query Match 59.5%; Score 342; DB 11; Length 214;  
Best Local Similarity 56.1%; Pred. No. 3.6e-29;  
Matches 60; Conservative 24; Mismatches 23; Indels 0; Gaps 0;

QY 4 DIOMIOSQKFMSTVGDVVTYTCASQNVGTN-VAMVQOKPGQSPNALIYSASYRSGVP 63  
DB 1 DIQTQSPSSMAYSLGERVITTCASQDINSYLSMFOQPKPSKTLITVRNRLVDGVP 60  
64 RFTGSGSGTDFTLITNVQSEDLADYFCQOQNSYPLFTGTGKLEIK 110  
61 RFGSGSGGODSLTISLSEEDMGIVYCYDDEPFTFGSGTKLEIK 107

RESULT 11  
Q9JL84 PRELIMINARY; PRT; 107 AA.

AC Q9JL84;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-BALB/C;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF206022; AAF69320.1; -.  
DR Interpro: IPR003006; -.  
DR Interpro: IPR003596; -.  
DR Pfam: PF00047; 1g; 1.  
DR SMART: SM00406; 1g; 1.  
FT NON\_TER 1  
FT NON\_TER 107 107

SO SEQUENCE 107 AA: 11648 MW: ACF9B1253ACA1E5D CRC64;

Query Match 56.2%; Score 323; DB 11; Length 107;

Best Local Similarity 56.1%; Pred. No. 1.7e-27;

Matches 60; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTVGDRTVTCASQNGTVNAMYQKPGOSPINALIYSASRYSGVPD 63  
 1 DIOMIOSQKFMSTVGDRTVTCASQNGTVNAMYQKPGOSPINALIYSASRYSGVPD 63

OY 64 RFTGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110  
 1 RFTGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110

DB 61 RFGSGSGXDYSLTISNLEPEDIATYCCQYNSKFPWTFCGKLEIK 107  
 1 RFGSGSGXDYSLTISNLEPEDIATYCCQYNSKFPWTFCGKLEIK 107

RESULT 12  
 OY0UL86 PRELIMINARY; PRT; 109 AA.

AC OY0UL86; PRELIMINARY; PRT; 109 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI\_TaxID=9606;

RA Young D.C.;

RA "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL: AF035028; AAD56264.1; -

DR HSSP: P01789; 1MCP.

DR InterPro: IPR003006; -

DR InterPro: IPR003596; -

DR Pfam: PF00047; 1g; 1.

DR SMART: SM00406; IGV; 1.

FT NON-TER 1 109

FT SEQUENCE 109 AA: 11928 MW: 243325F72C7DACC83 CRC64;

SO SEQUENCE 109 AA: 11928 MW: 243325F72C7DACC83 CRC64;

Query Match 54.9%; Score 315.5; DB 4; Length 109;

Best Local Similarity 55.6%; Pred. No. 1.1e-26;

Matches 60; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

OY 4 DIOMIOSQKFMSTVGDRTVTCASQNGTVNAMYQKPGOSPINALIYSASRYSGVP 62  
 1 DIOMIOSQKFMSTVGDRTVTCASQNGTVNAMYQKPGOSPINALIYSASRYSGVP 62

OY 63 DFTGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110  
 1 DFTGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110

DB 61 DRFGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 108  
 1 DRFGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 108

RESULT 13  
 OY0U410 PRELIMINARY; PRT; 106 AA.

AC OY0U410; PRELIMINARY; PRT; 106 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN

OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Rhabdiorhina; Neodermata;

OC Trematoda; Digenea; Strigeidae; Schistosomatidae; Schistosomatidae;

OC Schistosoma.

OX NCBI\_TaxID=6182;

RA SEQUENCE FROM N.A.

RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;

RT "Amplification, cloning and sequence analysis of the light chain

RT variable region gene of monoclonal anti-idiotypic antibody NP30 of

RT Schistosoma japonicum."

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL: AF207620; AAF19434.1; -

DR HSSP: P01679; 2FBJ.

DR InterPro: IPR003008; -

DR InterPro: IPR003006; -

DR InterPro: IPR003596; -

DR Pfam: PF00047; 1g; 1.

DR ProDom: PD000600; -; 1.

DR SMART: SM00406; IGV; 1.

FT NON-TER 1 106

FT SEQUENCE 106 AA: 11478 MW: F20F544426BAE63E CRC64;

SO SEQUENCE 106 AA: 11478 MW: F20F544426BAE63E CRC64;

Query Match 54.5%; Score 313.5; DB 5; Length 106;

Best Local Similarity 57.7%; Pred. No. 7.8e-26;

Matches 60; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

OY 7 MIOSQKFMSTVGDRTVTCASQNGTVNAMYQKPGOSPINALIYSASRYSGVPDRT 66  
 4 MIOSQKFMSTVGDRTVTCASQNGTVNAMYQKPGOSPINALIYSASRYSGVPDRT 66

OY 67 GSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110  
 1 GSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110

DB 63 GSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 106  
 1 GSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 106

RESULT 14  
 OY0YF0 PRELIMINARY; PRT; 298 AA.

AC OY0YF0; PRELIMINARY; PRT; 298 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE CN 8 SCFV.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RA SEQUENCE FROM N.A.

RA STRAIN-BALB/C; TISSUE-SPLEEN;

RA Shinozaki N., Demura T., Fukuda H.;

RT "Isolation of a novel type of vascular cell wall-specific monoclonal

RT antibody recognizing a cell polarity using a phase display subtraction

RT method."

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC EMBL: AB036341; BAA8633.1; -

DR HSSP: P01607; 1REI.

DR InterPro: IPR003006; -

DR InterPro: IPR003596; -

DR Pfam: PF00047; 1g; 2.

DR SMART: SM00406; IGV; 1.

SO SEQUENCE 298 AA: 31867 MW: E0F96B8A17004317 CRC64;

Query Match	53.9%	Score 310	DB 11	Length 298
Best Local Similarity	53.3%	Pred. No. 1.5e-25		
Matches 57	Conservative 19	Mismatches 31	Indels 0	Gaps 0

QY 4 DIQMISQKFMSTSVGDRVTYTCASQNVGTINAMYQKPGQSPNALITYASIRSYSPD 63  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 Db 173 DIEPTQSPASLASVGETVLTICRASGNIHNYLAMYQKQKQKSPDLLVYNAKTLADGVP 232

```

QY      64  RFTGSGSGTDFLTITNVQSEDLADYFCQOQNSYPLTFGTGKLEIK 110
      ||:||||| : : : || : : : : ||:|||||
Db      233  RFSGSGGTQYSLKINSLQPEDFGSYCCQHFMTTPYTFGGGTKLEIK 279

```

RESULT 15

PRELIMINARY; PRT; 104 AA.

DT	01-OCT-2000	(Tremblrel, 15, Created)
DT	01-OCT-2000	(Tremblrel, 15, Last sequence update)
DT	01-MAR-2001	(Tremblrel, 16, Last annotation update)
DE	ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BALB/C:	
RA	Malikiel S., Liao L., Cunningham M.W., Diamond B.;	
RT	"Characterization of cross-reactive monoclonal anti-myosin/anti-n-	
RL	acetyl-glucosamine antibodies from mice with autoimmune myocarditis."	
DR	Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.	
DR	EMBL; AF206024; AAF69322.1;	
DR	InterPro; IPR003006;	
DR	InterPro; IPR003596;	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; Icy; 1.	
FT	NON_TER	
FT	NON_TER	
FT	104	104
SQ	SEQUENCE	104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match	53.7%	Score 308.5	DB 11	Length 104
Best Local Similarity	57.8%	Pred. No. 6.1e-26		
Matches	59	Conservative	24	Indels 5
				Gaps 1

```
Oy      14 MSTSVGDRVYITCKASQ-----NVGTNVMAYQQKPGOSPINALITYSASYRYSGVDPRFTGS   68  
        : |::| ::::|::|       | |::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db      3 LPVSLGDQAISICRSRSDLVHTNGNTYLHMYLQKPQSPKLITYKVSNFSGVPDREFSGS   62
```

Qy 69 GSGTDFLTITNVQSEDLADYFCQQYNSYPLTFGTGKLEIK 110  
 ||||| |::||| ||| | ||| |||||  
 Db 63 GSGTDFLTIKISRVEAEDLCVYFCSQTHVPYTFGGGKLEIK 104

Search completed: June 20, 2001, 11:18:21  
Job time: 1842 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 11:18:56 ; Search time 33.18 Seconds  
(without alignments)  
113.566 Million cell updates/sec

Title: US-09-615-872-2

Perfect score: 575

Sequence: 1 AELDIQMIGSKFMSTSVGD.....CQOYNSYPLFTGCTKLEIK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	445	77.4	149 1 KV5A_MOUSE	P01633 mus musculu
2	400	69.6	136 1 KV5B_MOUSE	P01634 mus musculu
3	383	66.6	108 1 KV1M_HUMAN	P01605 mus sapien
4	383	66.6	108 1 KV1V_HUMAN	P04430 homo sapien
5	370	64.3	108 1 KV1Y_HUMAN	P80362 homo sapien
6	365	63.5	108 1 KV1E_HUMAN	P01510 homo sapien
7	361	62.8	108 1 KV1F_HUMAN	P01598 homo sapien
8	361	62.8	108 1 KV1G_HUMAN	P01599 homo sapien
9	358.5	62.3	107 1 KV1D_HUMAN	P01596 homo sapien
10	357	62.1	108 1 KV1L_HUMAN	P01604 homo sapien
11	357	62.1	108 1 KV1O_HUMAN	P01600 homo sapien
12	356	61.9	108 1 KV1J_HUMAN	P01608 homo sapien
13	356	61.9	108 1 KV1P_HUMAN	P01611 homo sapien
14	356	61.9	108 1 KV1S_HUMAN	P01607 homo sapien
15	352	61.2	108 1 KV1O_HUMAN	P01632 mus musculu
16	352	61.2	114 1 KV1A_MOUSE	P04431 homo sapien
17	352	61.2	129 1 KV1M_HUMAN	P04430 homo sapien
18	351.5	61.1	129 1 KV1H_HUMAN	P04430 homo sapien
19	351	61.0	114 1 KV4A_HUMAN	P01625 homo sapien
20	350	60.9	108 1 KV1B_HUMAN	P01594 homo sapien
21	347	60.3	134 1 KV4C_HUMAN	P01634 homo sapien
22	346	60.2	108 1 KV1A_HUMAN	P01593 homo sapien
23	345	60.0	108 1 KV1C_HUMAN	P01595 homo sapien
24	345	60.0	108 1 KV1N_HUMAN	P01606 homo sapien
25	343	59.7	108 1 KV1K_HUMAN	P01603 homo sapien
26	343	59.7	108 1 KV5K_MOUSE	P01644 mus musculu
27	342.5	59.6	133 1 KV4B_MOUSE	P06313 homo sapien
28	342	59.5	117 1 KV1I_HUMAN	P01601 homo sapien
29	341.5	59.4	129 1 KV1L_HUMAN	P18135 homo sapien
30	339.5	59.0	109 1 KV5J_MOUSE	P01622 mus sapien
31	339	59.0	108 1 KV5J_MOUSE	P01643 mus musculu
32	339	59.0	117 1 KV1J_HUMAN	P01602 homo sapien
33	338.5	58.9	129 1 KV3M_HUMAN	P18136 homo sapien

34	338	58.8	108 1 KV5L_MOUSE	P01645 mus musculu
35	338	58.8	128 1 KV5E_MOUSE	P01637 mus musculu
36	337	58.6	109 1 KV5P_MOUSE	P01649 mus musculu
37	336.5	58.5	109 1 KV3B_HUMAN	P01620 homo sapien
38	336.5	58.5	109 1 KV3F_HUMAN	P01624 mus musculu
39	336	58.4	108 1 KV5Q_MOUSE	P01650 mus musculu
40	335	58.3	108 1 KV1E_HUMAN	P01597 homo sapien
41	335	58.3	108 1 KV5S_MOUSE	P01652 mus musculu
42	335	58.3	108 1 KV5T_MOUSE	P01653 mus musculu
43	335	58.3	128 1 KV3K_HUMAN	P06311 homo sapien
44	334	58.1	108 1 KV5N_MOUSE	P01647 mus musculu
45	333	57.9	108 1 KV5D_MOUSE	P01636 mus musculu

## ALIGNMENTS

RESULT 1  
KV5A\_MOUSE STANDARD; PRT: 149 AA.  
ID KV5A\_MOUSE  
AC P01633;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-V REGION MPC11 PRECURSOR.  
OS Mus musculus (mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_Taxid=10090;  
RX [1]  
RP SEQUENCE OF 1-71 FROM N.A.  
RA MEDLINE=83001944; PubMed=6288267;  
RA Kelley D.E., Coleclough C., Perry R.P.;  
RT "Functional significance and evolutionary development of the  
RT 5'-terminal regions of immunoglobulin variable-region genes";  
RL Cell 29:681-689(1982).  
RN [2]  
RP SEQUENCE OF 41-149 FROM N.A.  
RA MEDLINE=80176554; PubMed=6245773;  
RA Rabbits T.H., Hamlyn P.H., Matthysens G., Roe B.A.;  
RT "The variability, arrangement, and rearrangement of immunoglobulin  
RT genes";  
RL Can. J. Biochem. 58:176-187(1980).  
RN [3]  
RP SEQUENCE OF 30-149.  
RA MEDLINE=78186617; PubMed=418775;  
RA Smith G.P.;  
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse  
RT myeloma MPC 11";  
RL Biochem. J. 171:337-347(1978).  
CC -I- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS  
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE  
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL  
CC RESIDUE OF TYPICAL KAPPA CHAINS.  
CC  
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CC or send an email to [license@sdb-sdb.ch](mailto:license@sdb-sdb.ch)).  
CC  
CC EMBL: J00561; AAA38776.1; -  
CC PIR: A01916; KVM511.  
CC Interpro: IPR003006; -  
CC pfam: pf00047; 19; 1.  
CC Immunoglobulin V region; Signal; Duplication.  
KW CHAIN 1 29  
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.  
FT DOMAIN 42 64 FRAMEWORK 1.  
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 76 90 FRAMEWORK 2.

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FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 98 129 FRAMEWORK 3.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 139 148 FRAMEWORK 4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SO SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match
Best Local Similarity 77.4%; Score 445; DB 1; Length 149;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTSVGDRVTCTCKASQNGTVNVMYQOKPGQSPNALIYSASRYSGVPD 63
DB 42 DIVMTQSHKFMSTSVGDRVTCTCKASQNGTVNVMYQOKPGQSPNALIYSASRYSGVPD 101
OY 64 RFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFGTGKLEIK 110
DB 102 RFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFGTGKLEIK 148

RESULT 2
KV5B_MOUSE STANDARD: PRT: 136 AA.
ID KV5B_MOUSE
AC P01634;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION MOPC 21 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Galt M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing."
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP SEQUENCE OF 30-136.
RA MEDLINE=73053310; PubMed=4638343;
RA Svasdi J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain."
RL Biochem. J. 128:427-444(1972).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: V00810; CAZ424192.1; ALT_TERM.
DR PIR: A01917; KMS21.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 29
FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.
FT DOMAIN 30 52 FRAMEWORK 1.
FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 64 78 FRAMEWORK 2.
FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 127 136 FRAMEWORK 4.
FT NON_TER 136 136
SO SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

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Query Match
Best Local Similarity 69.6%; Score 400; DB 1; Length 136;
Matches 80; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

OY 1 AELDIOMIOSQKFMSTSVGDRVTCTCKASQNGTVNVMYQOKPGQSPNALIYSASRYSG 60
DB 27 ADGNIVMTQSPKSMMSMSEGERVTLCTCKASENVTVNMYQOKPGQSPNALIYGASTREAGVPS 86
OY 61 VPDREFTGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFGTGKLEIK 110
DB 87 VPDREFTGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFGTGKLEIK 136

RESULT 3
KV1M_HUMAN STANDARD: PRT: 108 AA.
ID KV1M_HUMAN
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684(1976).
CC -----
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-II KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; KIHULY.
DR HSSD: P01607; IREI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 107 107 BY SIMILARITY.
FT NON_TER 108 108
SO SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match
Best Local Similarity 66.6%; Score 383; DB 1; Length 108;
Matches 70; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTSVGDRVTCTCKASQNGTVNVMYQOKPGQSPNALIYSASRYSGVPD 63
DB 1 DIOMIOSQKFMSTSVGDRVTCTCKASQNGTVNVMYQOKPGQSPNALIYGASTREAGVPS 60
OY 64 RFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFGTGKLEIK 110
DB 61 RFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFGTGKLEIK 107

RESULT 4
KV1V_HUMAN STANDARD: PRT: 108 AA.
ID KV1V_HUMAN

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AC P04430;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION BAN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=86174817; PubMed=3083240;  
 RA Dujlet F.E., O'Connor T.P., Benson M.D.;  
 RT "Polymorphism in a kappa I primary (Al) amyloid protein (BAN).";  
 RL Mol. Immunol. 23:73-78(1986).  
 DR PIR: A01878; KIHUBN.  
 DR HSSP: P80362; IWTL.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig: 1.  
 DR Immunoglobulin V region; Amyloid.  
 KW DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 1 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 66.6%; Score 383; DB 1; Length 108;  
 Best Local Similarity 66.4%; Pred. No. 2.3e-32;  
 Matches 71; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

OY 4 DIQMISQKFMSTVSGDRVTTCASQNVGTNAVYQKPGKPNLIYSASYSGVPD 63  
 DB 1 DIQMTSPSSLASVSGDRVTTCRASQSYNYVAMFQKPGKPKSLIDASTLQSGVPS 60  
 OY 64 RFTGSSGTDFTLTITNVOSEDLADYFCQOYNSPYLFTGTGLEIK 110  
 DB 61 NFGSGSGTDFLTITNVOSEDLADYFCQOYNSPYLFTGTGLEIK 107  
 NCBI\_TaxID=9606;

RESULT 5  
 KVIIR\_HUMAN  
 ID KVIIR\_HUMAN STANDARD; PRT; 108 AA.  
 AC P80362;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION WAT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RA MEDLINE=95086080; PubMed=7993911;  
 RA Huang D.-B., Chang C.-H., Alnsworth C., Bruenger A.T., Eultz M.,  
 RA Solomon A., Stevens F.J., Schiffer M.;  
 RT "Comparison of crystal structures of two homologous proteins:  
 RT structural origin of altered domain interactions in Immunoglobulin  
 RT light-chain dimers.";  
 RL Biochemistry 33:14848-14857(1994).  
 RN [2]  
 RP SEQUENCE OF 1-35.  
 RA MEDLINE=81267384; PubMed=6167731;  
 RA Stevens F.D., Westholm F.A., Panagiotopoulos N., Schiffer M.,  
 RA Popp R.A., Solomon A.;  
 RT "Characterization and preliminary crystallographic data on the VL-  
 RT related fragment of the human KI Bence Jones protein Wat.";

RL J. Mol. Biol. 147:185-193(1981).  
 CC -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
 DR PDB: 1WTL; 01-NOV-94.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig: 1.  
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 FRAMEWORK 3.  
 FT DOMAIN 57 88 FRAMEWORK 4.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 30 31 TN -> SD (IN REF. 2).  
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 64.3%; Score 370; DB 1; Length 108;  
 Best Local Similarity 62.6%; Pred. No. 4.8e-31;  
 Matches 67; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

OY 4 DIQMISQKFMSTVSGDRVTTCASQNVGTNAVYQKPGKPNLIYSASYSGVPD 63  
 DB 1 DIQMTSPSSLASVSGDRVTTCRASQSYNYVAMFQKPGKPKSLIDASTLQSGVPS 60  
 OY 64 RFTGSSGTDFTLTITNVOSEDLADYFCQOYNSPYLFTGTGLEIK 110  
 DB 61 NFGSGSGTDFLTITNVOSEDLADYFCQOYNSPYLFTGTGLEIK 107  
 NCBI\_TaxID=9606;

RESULT 6  
 KVIIR\_HUMAN  
 ID KVIIR\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01610;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION WEA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=83273707; PubMed=6410398;  
 RA Goni F., Frangione B.;  
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
 RT (protein WEA) with antibody activity against 3,4-pyruvylated  
 RT galactose in Klebsiella polysaccharides K30 and K33.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
 CC WALDENSTROM'S MACROGLOBULINEMIA.  
 DR PIR: A01876; KIHWE.  
 DR HSSP: P80362; IWTL.  
 DR InterPro: IPR003006;  
 DR Pfam: PF00047; Ig: 1.  
 KW Immunoglobulin V region; Monoclonal antibody.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 63.5%; Score 365; DB 1; Length 108;

Best Local Similarity 61.7%; Pred. NO. 1.5e-30;  
Matches 66; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

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QY      4 D I Q M I Q S Q K E N M S T S V E D R V T I T C A S Q N G T N V A M Q Q K P G C S P N A L I Y S A I R X S G V P D 63
      ||| || : ||||| : ||| : : ||||| : ||| : |||
Db      1 D I Q M T O S P S S L A S A V G D R V T I T C R A S Q G I R N D L T W Y Q Q K P G T A P K R L I Y G A T S L Q S G V P S 60

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QY      64 RFTGSGSGTPTLTITNVQSEDLADYEQQYNSTPLTEGTGRLEIK 110  
         ||::|||::|||:::||::|||::|||::|||::|||:  
Db      61 RFSGSGSGTEFTLLINSLAQPEDFAFYCQLQYSFPMTFGGQTRVEVK 107
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## RESULT 7

ID	KEY	VALUE	STATUS	DATE
AC	21-JUL-1986	rel. 01, Created	STANDARD	PRT, 108 AA.
DT	21-JUL-1986	rel. 01, Last sequence update		
DT	15-JUL-1999	rel. 38, Last annotation update		
DE	IG KAPPA CHAIN V-I REGION EU.			
OS	OS Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
ON	NCBI_TaxID=9606;			

RP	SEQUENCE.
RX	MEDLINE-71064023; PubMed-5489770;
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT	"The covalent structure of a human gamma G-immunoglobulin.VI. Amino acid sequence of the light chain.";
RL	Biochemistry 9:3155-3161(1970).
RN	[2]
RD	DISULFIDE BOND.
RX	MEDLINE-71064027; PubMed-4923144;
RA	Gall W.E., Edelman G.M.;
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
RL	Biochemistry 9:3188-3196(1970).
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
CR	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PRT:	A01866; KIHBU.
DR	HSSP: P01607; IRET.
DR	InterPro: IPR003006; ..
DR	Pfam: PF00047; 19; 1.
FT	KW Immunoglobulin V region.
FT	DOMAIN 1 23
FT	DOMAIN 24 34
FT	DOMAIN 35 49
FT	DOMAIN 50 56
FT	DOMAIN 57 88
FT	DOMAIN 89 97
FT	DOMAIN 98 107
FT	DOMAIN 108 108
FT	DISULFID 23 88
FT	NON_TER 108 108
SQ	SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D8823 CRC64;
Query Match	
Best Local Similarity 62.8%; Score 361; DB 1; Length 108;	
Matches 67; Conservative 17; Mismatches 23; Indels 0; Gaps	
OY	4 DIQMIO\$OKFMSTSVGDRVTVTCRASNQVNTGNVAMYQKRFQSGPNALISASRYRGVPD 633
DY	1 DIQMTPSPSTLASVGDRTVTITCRASQSIINLWLMAYQKPGKAPKLIMTKASLESGVPS 60
OY	64 RFGSGSGTDFLTITTNVQSGLADYPQQQNSNPFLFFGTGLEIK 110
DY	61 RFGSGSGTEFLTITSLDPDDFAITYCQDYNSDKMFGGGTVEVK 107
RESULT	8
ID	KYIG_HUMAN
ID	KYIG_HUMAN
STANDARD:	PRT: 108 AA.

AC P01599;  
DT 21-JUL-1986 (Rel. 01, Created)

CC	1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC	MARKER.
CC	1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2
RL	Eur. J. Biochem. 49:377-391(1974).
RT	"Primary structure of kappa light chain from a human myeloma
RA	protein";
RA	Malstein C.P., Deverson E.V.;
RA	MEDLINE=75075135; PubMed=4216454;
RP	SEQUENCE.
OX	NCBI_TaxID=9606;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON	[1]
DB	1 RFSGSGTDEFTLTITTTTINQSDADLADPCQOQYNSPLPFGTGTKEIK 110
DB	61 RFSGSGAGTEFTLTITSSLOPEDFATYVCLQONSXPBSFGQTKVEIK 107
DB	1 DIQMIOSQKFSTVSGRVYTCRASQNVGCTNVMVMOOKPGOSPNNALITYSASYRSGVPD 63
DB	1 DIQMIOSQSSLSASVGDPRVTITICRASQGRINDLWYQCKPEKAKRELITVYASNNQSGVPS 60
QY	4 DIQMIOSQKFSTVSGRVYTCRASQNVGCTNVMVMOOKPGOSPNNALITYSASYRSGVPD 63
QY	1 DIQMIOSQSSLSASVGDPRVTITICRASQGRINDLWYQCKPEKAKRELITVYASNNQSGVPS 60
QY	64 RFSGSGTDEFTLTITTTTINQSDADLADPCQOQYNSPLPFGTGTKEIK 110
QY	61 RFSGSGAGTEFTLTITSSLOPEDFATYVCLQONSXPBSFGQTKVEIK 107
RESULT 9	
KVID_HUMAN	
ID	KVID_HUMAN
AC	P01596;
AC	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG KAPPA CHAIN V-I REGION CAR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON	NCBI_TaxID=9606;
ON	[1]
RP	SEQUENCE.
RX	MEDLINE=75075135; PubMed=4216454;
RA	Malstein C.P., Deverson E.V.;
RA	"Primary structure of kappa light chain from a human myeloma
RT	protein";
RL	Eur. J. Biochem. 49:377-391(1974).
CC	1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2
CC	MARKER.
CC	1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC	PIR: A01864.K1HUAR.



DR HSP: P80362; 1MTL.  
 DR InterPro: IPR003006; -  
 KW Pfam: PF00047; 1g; 1.  
 DR Immunoglobulin V region; Glycoprotein.  
 FT CARBOHYD 28  
 FT NON\_TER 107 107 N-LINKED (GLCNAC. . .).  
 SQ SEQUENCE 107 AA; 11703 MW; EIBFODE9844C3346 CRC64;

Query Match 62.3%; Score 358.5; DB 1; Length 107;  
 Best Local Similarity 60.7%; Pred. No. 7e-30;  
 Matches 65; Conservative 21; Mismatches 20; Indels 1; Gaps 1;

OY 4 DIOMIOSQKFMSTVGDRVTYTCASQNVAVYQKPGOSPNALISATYRSGVPD 63  
 DB 1 DIOMTQSPSTLASVGDRAVITCRASQNSIMLAWYQKPKRAKXLYIKSSLSLEGVPS 60  
 OY 64 RFTGSGGTDFLTITNNVSEDLADYFCQOYNSYPLTFGTGTRKLEIK 110  
 DB 61 RFTGSGGTDFLTITNLSLAPBFAFYCCQYNTF-FTFGPGTKVDIK 106

RESULT 10  
 KY1L\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01604;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION KUE.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79237924; PubMed=112021;  
 RA Eultz M., Kley H.-P., Zeidler H.-J.;  
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid  
 sequence of the variable part of a human L-chain of the kappa-type.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR: A01870; KIHUKU.  
 DR HSP: P01607; 1RET.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; 1g; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 3 49 FRAMEWORK 2.  
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 5 57 FRAMEWORK 3.  
 FT DOMAIN 6 88 FRAMEWORK 4.  
 FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 8 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90AE98 CRC64;

Query Match 62.1%; Score 357; DB 1; Length 108;  
 Best Local Similarity 61.7%; Pred. No. 1e-29;  
 Matches 66; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTVGDRVTYTCASQNVAVYQKPGOSPNALISATYRSGVPD 63  
 DB 1 DIOMTQSPSTLASVGDRAVITCRASQNSIMLAWYQKPKRAKXLYIKASLTETGVPS 60  
 OY 64 RFTGSGGTDFLTITNNVSEDLADYFCQOYNSYPLTFGTGTRKLEIK 110  
 DB 61 RFTGSGGTDFLTITNLSLAPBFAFYCCQYNSYRPTFGGTRKLDIK 107

RESULT 11  
 KY1O\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01609;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION SCW.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75059271; PubMed=4435756;  
 RA Eultz M., Hilschmann N.;  
 RT "The primary structure of a human immunoglobulin L-chain of  
 kappa-type (Bence-Jones protein SCW.) II: The chymotryptic peptides  
 and the complete amino acid sequence.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR: A01875; KIHUSW.  
 DR HSP: P01607; 1RET.  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; 1g; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 3 49 FRAMEWORK 2.  
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 5 57 FRAMEWORK 3.  
 FT DOMAIN 6 88 FRAMEWORK 4.  
 FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 8 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match 62.1%; Score 357; DB 1; Length 108;  
 Best Local Similarity 59.8%; Pred. No. 1e-29;  
 Matches 64; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTVGDRVTYTCASQNVAVYQKPGOSPNALISATYRSGVPD 63  
 DB 1 DIOMTQSPSTLASVGDRAVITCRASQNSIMLAWYQKPKRAKXLYIKASLTETGVPS 60  
 OY 64 RFTGSGGTDFLTITNNVSEDLADYFCQOYNSYPLTFGTGTRKLEIK 110  
 DB 61 RFTGSGGTDFLTITNLSLAPBFAFYCCQYNSYRPTFGGTRKLEIK 107

RESULT 12  
 KY1L\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01600;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION HAU.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Matanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
 chain of subgroup I (Bence-Jones Protein Hau) : subdivision within  
 RT subgroups.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).



ID	NAME	STANDARD	PRT	108 AA
AD	KV10. HUMAN			
DT	P01607;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1996 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-I REGION REL.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE.			
RA	MEDLINE=76023758; PubMed=809329;			
RT	Palm W., Hilschmann N.;			
RT	"The primary structure of a crystalline monoclonal immunoglobulin			
RT	kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); isolation			
RT	and characterization of the tryptic peptides; the complete amino acid			
RT	sequence of the protein; a contribution to the elucidation of the			
RT	three-dimensional structure of antibodies, in particular their			
RT	combining site.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).			
RX	MEDLINE=76039968; PubMed=1182131;			
RA	Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;			
RT	"The molecular structure of a dimer composed of the variable portions			
RT	of the Bence-Jones protein REI refined at 2.0-A resolution.";			
RL	Biochemistry 14:4943-4952(1975).			
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)			
CC	MARKER.			
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR; A01873; KIHURE.			
DR	PDB; 1REI; 17-FEB-84.			
DR	InterPro; IPR003006; -.			
KW	Immunoglobulin V region; Bence-Jones protein; 3D-structure.			
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FT	DOMAIN	35	49	FRAMEWORK 2.
FT	DOMAIN	50	56	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	57	88	FRAMEWORK 3.
FT	DOMAIN	89	97	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	98	107	
FT	DISULFID	23	88	FRAMEWORK 4.
FT	STRAND	4	7	
FT	STRAND	10	13	
FT	TURN	15	16	
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FT	TURN	30	31	
FT	STRAND	33	38	
FT	TURN	40	41	
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QY      64 RFTSGSGDTFTLTITNVQSELDADYFCQQYNSTPLTFGTGKLEI 109
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Db      61 RFSGSGSDTYFTTISLQPEDIAITYYCQQYQLPYTFGGGTAKLI 106
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Search completed: June 20, 2001, 11:18:57  
Job time: 308 sec

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Best Local Similarity	61.3%	Pred. No. 3.2e-29;		
Matches 65;	Conservative 17;	Mismatches 24;	Indels 0;	Gaps 0;
4	DIQMOSKPFMTSGDGRVYTCRKSQNVGVNVAHQPGGSFNALLYSASTRYSGVD	63		



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1	514	89.4	107	2	A28195	Ig kappa chain V r	
2	498	86.6	107	2	B28195	Ig kappa chain V r	
3	496	86.3	128	2	A47159	Ig lambda chain V r	
4	484	84.2	108	2	PL0204	anti-DNA autoantibody	
5	475.5	82.7	108	2	B44371	Ig kappa chain V r	
6	474	82.4	98	2	PH1072	Ig light chain V r	
7	472	82.1	117	2	S42466	Ig kappa chain V r	
8	447	77.7	131	2	PL0207	Ig kappa chain V r	
9	445	77.4	107	2	S32192	anti-Idiotypic antibody	
10	445	77.4	149	1	KVMS11	Ig kappa chain V r	
11	443	77.0	107	2	S32191	Ig kappa chain V r	
12	439	76.3	100	2	H38601	Ig kappa chain V r	
13	439	76.3	119	2	PQ0265	Ig kappa chain V r	
14	425	73.9	88	2	A37262	Ig kappa chain V r	
15	417	72.5	152	2	S30751	Ig kappa chain V r	
16	413	71.8	127	2	S04577	Ig kappa chain V r	
17	412	71.7	90	2	S38561	Ig kappa chain V r	
18	410.5	71.4	108	2	PL0083	Ig light chain V r	
19	404	70.3	94	2	F33730	Ig kappa chain V r	
20	404	70.3	107	2	S059367	Ig kappa chain V r	
21	400	69.6	136	1	KVMS21	Ig kappa chain V-J	
22	399	69.4	111	2	D37266	Ig kappa chain V r	
23	398	68.2	90	2	I38601	Ig kappa chain V r	
24	392	68.2	93	2	S38559	Ig light chain V r	
25	392	68.0	132	2	S40334	Ig kappa chain V-J	
26	391	68.0	125	2	S40333	Ig kappa chain V r	
27	390	67.8	86	2	C28195	Ig kappa chain V r	
28	389	67.7	129	2	S40369	Ig kappa chain V r	
29	388.5	67.6	225	2	S37484	Ig kappa chain - n	

30	388	67.5	125	2	S40353	Ig kappa chain V-J
31	387	67.3	107	2	S38713	Ig light chain V r
32	385	67.0	107	2	I69017	anti-HIV1 envelope
33	385	67.0	125	2	S40349	Ig kappa chain V-J
34	384	66.8	117	2	S46371	Ig kappa chain V-J
35	383	66.6	108	1	K1HUX	Ig kappa chain V-I
36	383	66.6	108	1	K1HUBN	Ig kappa chain V-I
37	381	66.3	98	2	PHI073	Ig light chain V r
38	381	66.3	145	2	PL0014	Ig kappa chain pre
39	378	65.7	107	2	S31132	Ig kappa chain V r
40	377	65.6	123	2	S40313	Ig kappa chain V-J
41	377	65.6	129	2	S40317	Ig kappa chain - h
42	375.5	65.3	124	2	S40336	Ig kappa chain V-J
43	375	65.2	108	2	S36279	Ig lambda chain V
44	374	65.0	108	2	S40330	Ig kappa chain V-J
45	374	65.0	117	2	S40362	Ig kappa chain - h

## ALIGNMENTS

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RESULT      1
A28195
Ig kappa chain V region (anti-haloperidol antibody A) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C:Accession: A28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid
A:Reference number: A28195; MUID:88153717
A:Accession: A28195
A:Molecule type: mRNA
A:Residues: 1-107 <SHE>
A:Cross-references: GB:M19766; NID:q197039; PIDN:AAA38891.1; PID:q197040
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
C:16-90/Domain: Immunoglobulin homology <IM>

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Query Match	89.48;	Score 514;	DB 2;	Length 107;
Best Local Similarity	91.68;	Pred. No. 3.7e-38;		
Matches 98;	Conservative 3;	Mismatches 6;	Indels 0;	Gaps 0

[illegible]

## RESULT

Ig kappa chain V region (anti-haloperidol antibody B) - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 01-Dec-1999 #sequence\_revision 01-Dec-1989 #text\_change 21-Jan-2000  
C.Accession: B28195  
R.Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A.Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid  
A.Reference number: A28195; MUID:88153717  
A.Accession: B28195  
A.Molecule type: mRNA  
A.Residues: 1-107 <SHE>  
A.Cross-references: EMBL:M19767; NTD:G197041; PIDD:AAA38892.1; PJD:G197042  
C.Superfamily: immunoglobulin V region; immunoglobulin homology  
C.Keywords: heterotetramer; immunoglobulin  
C.Domain: immunoglobulin homology <IMM>  
C.Domain: immunoglobulin homology

Query match 86.68; Score 498; DB 2; Length 107;





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OY          4 DIOMISQKRMSTSVGDRTVYTCKASQNGTNAVYQCKPGOSPALLYSASYRSGVPD 63
            ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          42 DIWYOSHKKMSTSVGDRVSITCKASQDSVTVAWYQCKPGOSPALLYSASYRYTGVPD 101
OY          64 RFTGGSGGTDFELTLTNVQSEDLADVECGQNYSPLTPECTGKLEIK 110
            ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          102 RFTGGSGGTDFEPTLTISSVQAEDLAIVYCQOHSTPTEFGGKLEIK 148

RESULT      11
S32191
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32191
Rizul, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32191
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <107>
A:Cross-references: EMBL:X70095; NID:g288260; PIDN:CAA9700.1; PID:g288261
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
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Matches 85 ; Conservative 8 ; Mismatches 14 ; Indels 0 ; Gaps 0 ;

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Db  1 DIVVTGSKFKNSTSGDGVNLTCTKASQSDVSTAVAMVQKPGQSPALITYASRYTGVPD 60
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OY  64 RFTSGSGTDFLTITTVQSEDLADYFCQOQNSVPLFTFGTKLEIK 110
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  61 RFTSGSGTDFLTITTVQSEDLAVYYCOAHSTPYTFTGGGKLEIK 107
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12
H38601
Ig kappa chain V region (3A3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text-change 21-Jan-2000
C:Accession: H38601
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823
A:Accession: H38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <COS>
A:Cross-references: GB:557985; NID:g196416; PIND:AAA63366.1; PID:g196417
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
C:8-82/Domain: Immunoglobulin homology <IM>

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[illegible]

Db 61 TDFLTINSMGSEDLADYFCQGYSTYPECTFGGTRKLEIK 99

RESULT 13

P00265

Ig kappa chain V region (Mc1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000

C:Accession: P00265

R:Lothman, K.L., Carrillo, M.A.; Kennedy, R.C.

Gene 105, 283-284, 1991

A:Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal antibody

A:Reference number: P00265; MUID:92039046

A:Accession: P00265

A:Molecule type: mRNA

A:Residues: 1-119 <IOH>

A:Cross-references: GB:M59985

C:Comment: This protein recognizes a restricted idiotype associated with antibodies s

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:28-102/Domain: immunoglobulin homology <IMM>

F:36-46/Region: complementarity-determining 1

F:62-68/Region: complementarity-determining 2

F:101-109/Region: complementarity-determining 3

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Ig kappa chain V region (6H2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Aug-1991 #sequence\_revision 03-Apr-1992 #text\_change 09-May-1997  
C:Accession: A37262  
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A:Title: Common structural features among monoclonal antibodies binding the same antigen  
A:Reference number: A38601; MUID:91115823  
A:Accession: A37262  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-88 <GOS>  
A:Cross-references: GB:M57987  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

[illegible]





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Thu Jun 21 10:32:48 2001

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 11:14:11 : Search time 29.71 Seconds

(without alignments)  
74.585 Million cell updates/sec

Title: US-09-615-872-2

Perfect score: 575  
Sequence: 1 AELDIQMIQSQKFMSTSVGD.....CQGYNSYPLTFGTGKLEIK 110Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCRTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	517	89.9	127	4	US-08-646-265A-27	Sequence 27, Appl
2	514	89.4	107	4	US-08-767-128-32	Sequence 32, Appl
3	514	89.4	123	1	US-08-398-613A-20	Sequence 20, Appl
4	514	89.4	123	1	US-08-398-612A-20	Sequence 20, Appl
5	514	89.4	123	1	US-08-398-611A-20	Sequence 20, Appl
6	514	89.4	123	2	US-08-491-334A-20	Sequence 20, Appl
7	514	89.4	123	4	US-09-027-449-17	Sequence 17, Appl
8	514	89.4	123	4	US-08-804-444A-17	Sequence 17, Appl
9	514	89.4	123	4	US-09-026-985-17	Sequence 17, Appl
10	512	89.0	237	1	US-08-398-612A-28	Sequence 28, Appl
11	512	89.0	237	1	US-08-398-611A-28	Sequence 28, Appl
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14	512	89.0	237	4	US-08-804-444A-25	Sequence 25, Appl
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16	512	89.0	238	1	US-08-398-613A-28	Sequence 28, Appl
17	495.5	86.2	110	2	US-08-602-725-2	Sequence 2, Appl
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19	493.5	85.8	124	3	US-08-466-151-4	Sequence 5, Appl
20	490	85.2	131	3	US-08-202-047-5	Sequence 5, Appl
21	490	85.2	131	3	US-08-964-690-5	Sequence 5, Appl
22	488.5	85.0	110	1	US-08-497-312-23	Sequence 23, Appl
23	475.5	82.7	110	1	US-08-497-312-28	Sequence 29, Appl
24	474	82.4	126	4	US-08-646-265A-81	Sequence 81, Appl
25	471.5	82.0	108	2	US-08-657-012-25	Sequence 25, Appl
26	471.5	82.0	108	3	US-09-013-872-25	Sequence 25, Appl
27	471.5	82.0	108	4	US-09-184-198-25	Sequence 25, Appl

28	467	81.2	107	1	US-08-491-845-4	Sequence 4, Appl
29	467	81.2	147	2	US-08-653-402B-4	Sequence 4, Appl
30	466	81.0	126	4	US-08-646-265A-73	Sequence 73, Appl
31	464.5	80.8	110	1	US-08-497-312-25	Sequence 25, Appl
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36	464	80.7	132	2	US-08-452-164A-55	Sequence 55, Appl
37	463	80.5	237	2	US-08-926-789-16	Sequence 16, Appl
38	463	80.5	237	2	US-08-926-789-16	Sequence 16, Appl
39	463	80.5	241	2	US-08-224-591-18	Sequence 18, Appl
40	463	80.5	241	2	US-08-926-789-18	Sequence 18, Appl
41	459	79.8	126	4	US-08-646-265A-69	Sequence 69, Appl
42	459	79.8	126	4	US-08-646-265A-75	Sequence 75, Appl
43	456	79.3	107	3	US-08-554-840-3	Sequence 3, Appl
44	455	79.1	107	4	US-08-646-265A-131	Sequence 131, App
45	455	79.1	126	4	US-08-646-265A-85	Sequence 85, Appl

## ALIGNMENTS

RESULT 1  
US-08-646-265A-27  
; Sequence 27, Application US/08646265A  
; Patent No. 6214973  
; GENERAL INFORMATION:  
; APPLICANT: OHTOMO, Toshihiko  
; APPLICANT: SATO, Koh  
; APPLICANT: TSUCHIYA, Masayuki  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,265A  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP94/01763  
; FILING DATE: 19-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-291078  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25, 258  
; REFERENCE/DOCKET NUMBER: 53466/184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELE: 904136  
; INFORMATION FOR SEQ ID NO.: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-646-265A-27



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1  APPLICANT: Kim, Kyung Jin
2  APPLICANT: Leong, Steven R.
3  TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
4  TITLE OF INVENTION: Of Inflammatory Disorders
5  NUMBER OF SEQUENCES: 58
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Genentech, Inc.
8  STREET: 460 Point San Bruno Blvd
9  CITY: South San Francisco
10 STATE: California
11 COUNTRY: USA
12 ZIP: 94080
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Winpatin (Genentech)
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/398, 611A
22 FILING DATE: 01-Mar-1995
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/205864
26 FILING DATE: 03-MAR-1994
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Love, Richard B.
29 REGISTRATION NUMBER: 34,659
30 REFERENCE/DOCKET NUMBER: P0874P1
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 415/225-5530
33 TELEFAX: 415/952-9881
34
35 TELEX: 910/371-7168
36 INFORMATION FOR SEQ ID NO: 20:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 123 amino acids
39 TYPE: Amino acid
40 TOPOLOGY: Linear
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42 US-08-398-611A-20
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PRIOR APPLICATION DATA:

US-08-804-444A-17

Query Match	89.48;	Score 514;	DB 4;	Length 123;
Best Local Similarity	90.78;	Pred. No. 2.8e-42;		

```

1 APPLICANT: Hebert, Caroline Alice
2 APPLICANT: Kim, Kyung Jin
3 APPLICANT: Leong, Steven R.
4 TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
5 TITLE OF INVENTION: Treatment of Inflammatory Disorders
6 NUMBER OF SEQUENCES: 58
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Genentech, Inc.
9 STREET: 460 Point San Bruno Blvd
10 CITY: South San Francisco
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94080
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: WinPatIn (Genentech)
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/398,612A
22 FILING DATE: 01-MAR-1995
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/398611
26 FILING DATE: 01-Mar-1995
27 APPLICATION NUMBER: 08/205864
28 FILING DATE: 03-MAR-1994
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Love, Richard B.
31 REGISTRATION NUMBER: 34,659
32 REFERENCE/DOCKET NUMBER: P0874P1
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 415/225-5530
35 TELEFAX: 415/952-9881
36 TELEX: 910/371-7168
37 INFORMATION FOR SEQ ID NO: 28:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 237 amino acids
40 TYPE: Amino Acid
41 TOPOLOGY: Linear
42
43 US-08-398-612A-28
44
45 Query Match      89.0%; Score 512; DB 1; Length 237;
46 Best Local Similarity 88.2%; Pred.No. 9.2e-42;
47 Matches 97; Conservative 6; Mismatches 7; Indels 0; Gaps 0
48
49 QY 1 AELDIQMIOQKFMSTSVGDRVTYTCCKASQNNGTNVAMTQQKPGOSPALLITSASRYSG 60
50   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 Db 21 AYADIVMROSQKFMTSGVDKRVSYTCCKASQNNGTNVAMTQQKPGOSPALKIYSSSYRYS 80
52
53 QY 61 VPDRTGGSGGTDFLTITNVOSEDLADYFCOOVNSYPLTFEFGTKLEIK 110
54   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
55 Db 81 VPDRTGGSGGTDFLTITSHVOSEDLADYFCOOVNIPLTFEPGTKLEIR 130
56
57 RESULT 11
58 US-08-398-611A-28
59 Sequence 28, Application US/08398611A
60 Patent No. 5702946
61 GENERAL INFORMATION:
62 APPLICANT: Doershuk, Claire M.
63 APPLICANT: Fong, Sherman
64 APPLICANT: Hebert, Caroline Alice
65 APPLICANT: Kim, Kyung Jin
66 APPLICANT: Leong, Steven R.
67 TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
68 TITLE OF INVENTION: of Inflammatory Disorders
69 NUMBER OF SEQUENCES: 58
70 CORRESPONDENCE ADDRESS:
71 ADDRESSEE: Genentech, Inc.
72 STREET: 460 Point San Bruno Blvd
73 CITY: South San Francisco

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	RESULT	ALIGNMENTS
XX	Y44991 standard; Protein: 450 AA.	
XX	Y44991	
AC	Y44991:	
XX	23-MAY-2000 (first entry)	
DE	M79scFv-Interleukin 2-fusion protein containing dimerisation domain.	
XX		
KW	Murine; M79 antibody; 17-1A antigen: single-chain Fv fragment; scFv;	Murine monoclonal
KW	fusion construct; human; Interleukin 2; IL-2; dimerisation domain;	Anti IL-8 monoclon
KW	heteroantibody: multifunctional compound; constant domain;	Murine 5.12.14 ant
KM	immunoglobulin; cytosolic; immunostimulatory; anti-leukaemia; diagnosis;	Murine anti-IL-8 a
KW	anti-proliferative; prevention; treatment; malignant; haematopoietic cell;	Murine anti-IL-8 e
KM	Lymphoma; Leukaemia; solid tumour; carcinoma; melanoma; sarcoma.	Anti-IL-8 Mab 5.11-hum
XX		Murine variable an
OS	Chimeric - Mus sp.	Chimeric anti IL-6-
OS	Chimeric - Homo sapiens.	Chimeric monoclonal
XX		Anti-IL-8 mouse-hu
FH	Key	Mab 5.12.14 and hu
FT	Peptide	Chimeric anti IL-6-
FT	/label= Leader_peptide	5.12.14 L chain v
FT	Region	Chimeric anti-IL-8-
FT	/label= M79scFv_light_chain_variable_region	Variable region of
FT	Region	hCEA specific mous
FT	/label= gly_Ser-linker	Murine 708 VI amin
FT	Region	2A2 Human IgG4 exp
FT	/label= M79scFv_heavy_chain_variable_region	Murine anti-porc
FT	additional residues"	Murine P1A3 monoc
FT	269..303	P1A3 antibody kap
FT	/label= DHLX-dimerisation_domain	MEI3 light chain
FT		Light chain amino
FT		Mouse PAP recepto
FT		Human CD30 bindin
FT		Monoclonal antibod
FT		Protein sequence c
FT		Light chain V reg
FT		Mouse PAP recepto
FT		Variable light sub
FT		Antibody 24-31 hum
FT		chIRg4.12 L6 ligh

Query Match	Best Local Similarity	Score	DB	Length
Matches 100: Conservative	92.3%;	531;	DB 21;	450;
	Pred. No. 1.2e-37;			
	Mismatches 4;	Indels 0;	Gaps 0	
Oy	4	DIQMOSQKFMSTVSGDRVTYVTKASQNVGTNVAWTQKRGSGSPNALITYASSTRYSQVDP	63	
Db	20	dlqltqtsqgkfmstsvgydrsvtckasqnytnavaygkpgsgpalkllysaasyrgsvdp	79	
Oy	64	RFTGSGSGGDFLTITTNVOSDLDADVFCCOYNYSYPLTFEGTGLEIK	110	
Db	80	rltgsqsgtdfltltsnvgseadiaefcqdqymypilrtfgatkleik	126	

DE	23-MAY-2000	(first entry)
XX	M79scFv-interleukin 2-fusion protein containing tetramerisation domain.	
XX		
KW	Murine; M79 antibody; 17-1A antigen; single-chain Fv fragment; scFv; fusion construct; human; interleukin 2; IL-2; tetramerisation domain;	
KW	heteromolecule; multifunctional compound; constant domain;	
KW	immunoglobulin; cytosolic; immunostimulatory; antileukaemia; diagnosis;	
KW	antiproliferative; prevention; treatment; malignant; leukaemia; sarcoma.	
KW	Lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.	
XX		
OS	Chimeric - Mus sp.	
OS	Chimeric - Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/label= Leader_peptide
FT	Region	20..126
FT		/label= M79scFv_light_chain_variable_region
FT	Region	127..141
FT		/label= Gly-Ser_Linker
FT	Region	142..256
FT		/label= M79scFv_heavy_chain_variable_region
FT	Region	257..269
FT		/note= "Human IgG3 upper hinge region with additional residues"
FT	Domain	270..308
FT		/label= Human_p53_tetramerisation_domain
FT	Peptide	309..315
FT		/label= Short_peptide_linker
FT	Domain	316..450
FT		/label= Interleukin-2_domain
FT	Region	451..456
FT		/label= His_tag
XX		
PN	WO200006605-A2.	
XX		
PD	10-FEB-2000.	
XX		
PF	28-JUL-1999;	99WO-EP05416.
XX		
PR	28-JUL-1998;	98EP-0114082.
XX		
PA	(M1CR-) MICROMET GBS BIOMEDIZINISCHE FORSCHUNG.	
PI	Kuifer P, Dreier T, Baerle PA, Borschert K, Zettl F;	
XX		
DR	WPI: 2000-195265/17.	
XX		
DR	N-PSDB: Z50585.	
XX		
PT	New multifunctional compounds useful for preventing and/or treating	
PT	malignant cell growth and for detection and diagnosis	
XX		
PS	Example 9; Fig 48; 166pp; English.	
XX		
CC	The patent discloses heteromolecules which are multifunctional compounds	
CC	producible in a mammalian host cell as a secretable and fully functional	
CC	heterodimer of two polypeptide chains, where one of the polypeptide	
CC	chains comprises, a C1-domain (constant domain of an immunoglobulin	
CC	heavy chain) and the other chain comprises C2-domain (constant domain of	
CC	an immunoglobulin light chain). The polypeptide chains further comprise,	
CC	fused to the constant domains at least two (poly)peptides having	
CC	different receptor or ligand functions, where further at least two of the	
CC	different (poly)peptides lack an intrinsic affinity for one another and	
CC	are linked via the constant domains. The heteromolecules have	
CC	cytostatic, immunostimulatory, antileukaemia and antiproliferative	
CC	activities. These compounds can be used for diagnosing, preventing and	
CC	treating malignant cell growth related to malignancies of hematopoietic	
CC	cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,	
CC	melanomas and sarcomas.	
CC	The present sequence is a fusion protein comprising murine	
CC	17-1A-antigen specific M79 single-chain Fv (scFv) fragment at the	
CC	N-terminus, human interleukin-2 at the C-terminus and a tetramerisation	

CC used in the construction of an expression vector, contg. cDNA





FT	Region	90..98	"complementarity determining region (CDR) as indicated by Kabat sequence comparison"
FT		/note=	
FT	Region	92..98	"complementarity determining region (CDR) as indicated by X-ray crystallography"
FT		/note=	
XX	US5686070-A.		
XX	11-NOV-1997.		
XX	01-MAR-1995;	95US-0398612.	
XX	01-MAR-1995;	95US-0398612.	
XX	03-MAR-1994;	94US-0205864.	
PA	(GETH ) GENENTECH INC.		
PA	(INDV ) UNIV INDIANA.		
PI	Doerschuk CM, Fong S, Hebert CA, Kim KJ, Leong SR;		
DR	WPI: 1997-558085/51.		
DR	N-PsDB: V03200.		
PT	Treatment of bacterial pneumonia - with monoclonal antibody specific for interleukin-8; inhibits lung inflammatory conditions		
PS	Claim 5; Fig 16; 63pp; English.		
CC	The present sequence represents the light chain variable region of the monoclonal antibody 5.12.14. This antibody is a murine anti interleukin-8 (IL-8) IgG2a isotype. IL-8 is a neutrophil chemotactic peptide secreted by a variety of cells in response to inflammatory mediators. IL-8 can play an important role in the pathogenesis of inflammatory disorders such as adult respiratory distress syndrome (ARDS), septic shock and multiple organ failure. Treatment of bacterial pneumonia in a mammal comprises administering an anti IL-8 monoclonal antibody, such as 5.12.14., that binds human IL-8 with a Kd of 10-8 to 10-11 M, inhibits neutrophil chemotaxis in response to IL-8, inhibits IL-8 mediated elastase release by neutrophils and does not bind to C5a, beta-TG or platelet factor 4. IL-8 specific monoclonal antibodies are especially useful for treating pneumonia caused by Streptococcus pneumoniae, E. coli or Pseudomonas aeruginosa in humans. The antibodies may also be used in the treatment of ulcerative colitis and other inflammatory conditions.		
SO	Sequence 123 AA:		
	Query Match	89.4%;	Score 514; DB 18; Length 123;
	Best Local Similarity	90.7%;	Pred. No. 8.7e-37;
	Matches 97; Conservative	5; Mismatches 5; Indels 0; Gaps 0.	
OY	4 DIOMOSQKPFMTSTVGSDRTVTCKASQNVAVNVOOKPQGSPNALITYSASYRSQGVDP 63   Db 1 diwmqskrkmsctsvgdrtvsvckkassqnrvnvaayqgdpqpsxpallyssysrysgvpd 60		
OY	64 RFTGSQSGTDFLTITTNVQSEDLAFVFCOVNSYPLTFGTGTRLEIK 110   Db 61 rftgsqsgtfdltitshvqsedladyfcqgnilypltfpgpkyleik 107		
RESULT	9		
ID	W31574		
XX	W31574 standard; Protein: 123 AA.		
AC	W31574;		
DT	24-FEB-1998 (first entry)		
XX	Anti IL-8 monoclonal antibody (5.12.14) light chain variable region.		
XX	murine light chain; 5.12.14; human interleukin-8; IL-8; anti IL-8;		

[illegible]



CC	antibody Anti-IL-8 antibodies are especially used to treat or prevent
CC	allergic asthma in humans. They inhibit: (a) neutrophil chemotaxis in
CC	response to IL-8; (b) IL-8-mediated release of elastase from neutrophils
CC	and (c) binding of IL-8 to neutrophils. Anti-IL-8 antibodies can be used
CC	to treat many other inflammatory disorders, e.g. ischaemic reperfusion,
CC	ARDS, dermatitis, particularly bacterial pneumonia and inflammatory
CC	bowel disease.
XX	
XX	Sequence      123 AA:
SQ	
Query Match	89.4% Score 514; DB 18; Length 123;
Best Local Similarity	90.7%; Pred. No. 8.7e-37;
Matches 97; Conservative	5; Mismatches 5; Indels 0; Gaps 0;
OY	4 DIQMIOSEKFMSTVSGDVRVTCKASQNWGTNVAWYQQKPCGSPNALIYSASYRSGVPD 63   1 dlvmtgqskfnstsvgdvrvctckasqvngvnwagqkpgpsphallyssasyrsgvpd 60
OY	64 RFTGSGETDFTLTITTNVQSEDLADYFCQOYNSTPLRTGTKEIK 110   61 rftgsgetdftltitshvsqedladyfcqynystplrtgtptkleik 107
RESULT 11	
ID	W69305 standard; Protein; 123 AA.
XX	
AC	W69305;
XX	
DT	15-FEB-1999 (first entry)
DE	Murine anti-IL-8 Mab 5.12.14 light chain.
XX	
KW	Humanised antibody; monoclonal antibody; mouse; interleukin-8;
KW	inflammation; immunotherapy; therapy; psoriasis;
KW	inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW	ischaemic reperfusion; adult respiratory distress syndrome;
KW	dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
KW	rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
KW	leukocyte diapedesis; multiple organ injury syndrome; septicæmia;
KW	trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
KW	vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis.
XX	
OS	Mus sp.
XX	
FH	Location/Qualifiers
FT	/note= "light chain variable region"
FT	110..123
FT	/note= "constant region"
FT	24..34
FT	/label= CDR1
FT	/note= "complementarity determining region
FT	determined by Kabat sequence comparison"
FT	26..32
FT	/label= CDR1
FT	/note= "complementarity determining region
FT	determined by X-ray crystallography"
FT	50..56
FT	/label= CDR2
FT	/note= "complementarity determining region
FT	determined by Kabat sequence comparison"
FT	50..52
FT	/label= CDR2
FT	/note= "complementarity determining region
FT	determined by X-ray crystallography"xx
FT	89..97
FT	/label= CDR3
FT	/note= "complementarity determining region
FT	determined by Kabat sequence comparison"
FT	91..97
FT	/label= CDR3
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FT /note= "complementarity determining region  
FT determined by X-ray crystallography"  
KW MO9837200-A2.  
PN 27-AUG-1998.  
XX  
XX  
XX 20-FEB-1998; 98WO-US03337.  
XX  
XX 22-JAN-1998; 98US-0012116.  
XX 21-FEB-1997; 97US-0804444.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Hsai V, Koumenis I, Leong SR, Presta LR, Shahrokh Z;  
PI Zapata GA;  
XX  
XX WPI: 1998-467563/40.  
XX  
XX N-PSDB: V55092.  
XX  
XX  
XX New conjugates of antibody fragments - having covalently attached  
PT non-proteinaceous polymer molecules, particularly polyethylene  
PT glycol, for improving the residence time in the circulation.  
XX  
XX  
XX Example C: Fig 16; 328pp; English.  
XX  
XX This polypeptide comprises the light chain variable region and part  
CC of the constant light region of murine anti-interleukin-8 (IL-8)  
CC monoclonal antibody (Mab) 5.12.14. CDNA (see V55092) encoding this  
CC polypeptide was obtained by PCR amplification (see V55080-83) of  
CC hybridoma ATCC HB 11722 CDNA. Humanised anti-IL-8 Mabs and variants  
CC are described for use in diagnostic applications and in the  
CC treatment of inflammatory disorders. The invention provides  
CC conjugates of an antibody fragment and a polymer, such as PEG, that  
CC have improved half-life, mean residence time, and/or clearance  
CC rate. The conjugates can be used for immune therapy of e.g.  
CC psoriasis, responses associated with inflammatory bowel disease  
CC (such as Crohn's disease and ulcerative colitis), ischemic  
CC reperfusion, adult respiratory distress syndrome, dermatitis,  
CC meningitis, encephalitis, uveitis, autoimmune diseases such as  
CC rheumatoid arthritis, Sjogren's syndrome, vasculitis, diseases  
CC involving leukocyte diapedesis, central nervous system inflammatory  
CC disorder, multiple organ injury syndrome secondary to septicemia  
CC or trauma, alcoholic hepatitis, bacterial pneumonia, antigen-antibody  
CC complex mediated diseases, inflammations of the lung, including  
CC pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis,  
CC bronchiectasis, and cystic fibrosis.  
XX  
XX Sequence 123 AA;  
SQ

Query Match 89.4%; Score 514; DB 19; Length 123;  
Best Local Similarity 90.7%; Pred. No. 8.7e-37;  
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 DIQMOSQKFMSTVGDRTVTCKASQNVGVNMYQOKPGOSPMALYASIRSGVPD 63  
DB 1 dlvmtqskfmsvgydvsvckasqnvgtvayyqkpgpskpalysyrsygvpd 60  
QY 64 RTGSGSGDFLTITTVNOSDLADYPCQOVNSYPLTFETGKLEIK 110  
DB 61 rftgsqsgdfiltitvnsedladycqyniyltftgpkleik 107

RESULT 12  
W40120  
ID W40120 standard; protein; 123 AA.  
XX  
XX W40120;  
AC  
XX 03-JUN-1998 (first entry)  
DT  
XX Murine monoclonal antibody 5.12.14 light chain variable region.  
DE

XX Monoclonal antibody; Mab 5.12.14; interleukin-8; IL-8; anti-IL-8; murine;  
KW ulcerative colitis; immunotherapy; bacterial pneumonia; variable region;  
KW treatment; light chain; heavy chain; neutrophil chemotaxis inhibitor;  
XX  
XX Mus sp.  
XX  
XX Location/Qualifiers  
FH Key 1..109  
FT Region /note= "murine variable light region"  
FT 24..34  
FT Region /label= CDR\_#1  
FT /note= "alternative complementarity determining  
FT region #1"  
FT 26..32  
FT Region /label= CDR\_#1  
FT /note= "complementarity determining region #1"  
FT 50..52  
FT Region /label= CDR\_#2  
FT /note= "complementarity determining region #2"  
FT 50..56  
FT Region /label= CDR\_#2  
FT /note= "alternative complementarity determining  
FT region #2"  
FT 91..97  
FT Region /label= CDR\_#3  
FT /note= "complementarity determining region #3"  
FT 89..97  
FT Region /label= CDR\_#3  
FT /note= "alternative complementarity determining  
FT region #3"  
FT 110..123  
FT Region /note= "partial murine constant light region"  
XX  
XX US5707622-A.  
XX  
XX 13-JAN-1998.  
XX  
XX 01-MAR-1995; 95US-0396851.  
XX  
XX 01-MAR-1995; 95US-0396851.  
XX 03-MAR-1994; 94US-0205864.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Fong S, Hebert CA, Kim KJ, Leong SR;  
PI  
XX  
XX WPI: 1998-100296/09.  
XX N-PSDB: V10286.  
XX  
XX Immunotherapy of ulcerative colitis - with monoclonal antibody  
PT specific for interleukin-8  
XX  
XX Claim 7; Fig 16; 63pp; English.  
XX  
XX This sequence represents the light chain variable region of the murine  
CC 5.12.14 (anti-IL-8) monoclonal antibody (Mab) which is used in the  
CC construction of the plasmid pAS1214LV. This plasmid is used in a novel  
CC method for treating ulcerative colitis which involves the administration  
CC of an anti-IL-8 monoclonal antibody capable of binding to human  
CC interleukin-8 (IL-8) with a Kd of 10-8 to 10-11 M. This Mab also  
CC inhibits neutrophil chemotaxis in response to IL-8, inhibits  
CC IL-8-mediated elastase release by neutrophils and does not bind to C5a,  
CC beta-TG or platelet factor 4. The anti-IL-8 antibodies can also be used  
CC for the treatment of bacterial pneumonia.  
XX  
XX Sequence 123 AA;  
SQ

Query Match 89.4%; Score 514; DB 19; Length 123;  
Best Local Similarity 90.7%; Pred. No. 8.7e-37;  
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY	4	DIQIOSKPEFSTVGBDVFVTCASQNVGNVAMVQOKRGQSPNALIYSASVRYSGVPD	63
Db	1	divmtgskfmsvsgdvtvscasqnvgnvawwyqdkp9gskpalkaliysssyrysgvpd	60
QY	64	RFTGSGSGTDFLTITVTVQSEDLADVFCQOYNSYPLTFGTGKLEIK	110
Db	61	rftgsgsgtdftltlshvsgedladycqgnlypltfpgtklelk	107
RESULT	13		
ID	W33739	standard; Protein; 123 AA.	
XX	XX	W33739;	
XX	XX	01-MAY-1998 (first entry)	
DE	XX	Anti IL-8 monoclonal antibody (5.12.14) light chain variable region.	
XX	XX	murine light chain; 5.12.14; human interleukin-8; IL-8; anti IL-8;	
KW	XX	monoclonal antibody; diagnosis; inflammatory disorder; treatment;	
KW	XX	pneumonia; complementarity determining region; CDR; variable region;	
KW	XX	constant region; chimeric; ulcerative colitis.	
OS	XX	Mus sp.	
XX	XX	Location/Qualifiers	
FT	FT	1..109	
FT	FT	/note-	
FT	FT	Region	
FT	FT	24..34	
FT	FT	/note-	
FT	FT	Region	
FT	FT	26..32	
FT	FT	/note-	
FT	FT	Region	
FT	FT	50..56	
FT	FT	/note-	
FT	FT	Region	
FT	FT	50..52	
FT	FT	/note-	
FT	FT	Region	
FT	FT	89..97	
FT	FT	/note-	
FT	FT	Region	
FT	FT	91..97	
FT	FT	/note-	
FT	FT	Region	
FT	FT	110..123	
FT	FT	/note-	
XX	XX	US5702946-A.	
PN	XX	30-DEC-1997.	
XX	XX	01-MAR-1995; 95US-0398611.	
XX	XX	01-MAR-1995; 95US-0398611.	
XX	XX	03-MAR-1994; 94US-0205864.	
XX	XX	(GETH ) GENENTECH INC.	
XX	XX	Doerschuk CM, Fong S, Hebert CA, Kim KJ, Leong SR;	
XX	XX	WPI: 1998-076425/07.	
DR	XX	N-PSDB: V06411.	
XX	XX	Monoclonal antibody specific for interleukin-8 - used for treating	
PT	XX	IL-8 mediated inflammatory diseases, e.g. ulcerative colitis	
XX	XX	Disclosure; Fig 16; 63pp; English.	
XX	XX	This is the light chain variable region and a partial constant region	
CC	CC	of the murine monoclonal antibody 5.12.14. The variable region comprises	

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CC of complementarity determining regions (CDR). The encoding cDNA was
CC cloned into vector pBl3.1 to construct pA512i4VL which was used in the
CC construction of a chimeric 5.12.14 Fab vector by various recombinant
CC techniques. This chimeric Fab comprises of CDRs of a light chain and/or
CC a heavy chain variable region from the murine species and light chain
CC and/or heavy chain constant region of the human immunoglobulin IgG1.
CC This recombinant human-murine chimeric Fab has ant interleukin-8 (IL-8)
CC activity and can inhibit the IL-8 binding to human neutrophils. This
CC anti IL-8 Fab can be used for diagnosis of interleukin-8 mediated
CC inflammatory diseases and in the treatment of ulcerative colitis and
CC bacterial pneumonia.
XX
SQ Sequence 123 AA;

Query Match 89.4%; Score 514; DB 19; Length 123;
Best Local Similarity 90.7%; Pred. No. 8.7e-37;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 4 DIQMIOQKFNSTSGDRYTYCKRKSQNVGVNVAHQKRGQSPNALITASATRSIGVD 63
   |||
Db 1 divmvqskkfmsvsgdvsvyckasqnvglvavwyqkpgqspkallyssrysgvdp 60
   |||

OY 64 RPTGSGSGTDFLTITTNVQSEDLAVFCQOQYNSYPLTFCGTGKLEIK 110
   |||
Db 61 rftgsqsgldflltshvgsedladyfcqgnyilptlftpgytkleik 107
   |||

RESULT 14
Y29437
ID Y29437 standard; Protein; 123 AA.
XX
AC Y29437;
XX
DT 05-OCT-1999 (first entry)
XX
DE Murine 5.12.14 anti-IL-8 monoclonal antibody fragment.
XX
KW Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
XX diagnosis; inflammatory disorder; conjugate; immunoglobulin.
XX
OS Mus musculus.
XX
PN W09937779-A1.
XX
PD 29-JUL-1999.
XX
PE 19-JAN-1999; 99WO-US01081.
XX
PF 24-JUL-1998; 98US-0122513.
XX
PR 22-JAN-1998; 98US-0012116.
XX
PR 20-FEB-1998; 98WO-US03337.
XX
PR 24-JUL-1998; 98US-021952.
XX
PA (GETH ) GENENTECH INC.
XX
PI Hseil V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;
PI Zapata GA;
XX
WP: 1999-469134/39.
DR N-PSDB; X90558.
XX
CC New conjugates of nonproteinaceous polymers with antibody fragments,
CC used for treating inflammatory disorders
XX
XX Example; Fig 16: 360pp; English.
XX
CC The present invention describes a novel conjugate having one or more
CC antibody fragments covalently attached to one or more nonproteinaceous
CC polymer molecules, where the apparent size of the conjugate is at least
CC about 500 kDa. Conjugates of antibody fragments which bind the human
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC treating inflammatory disorders e.g. acute lung injury, ischaemic

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